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OM protein - protein search, using sw model

Run on: March 2, 2005, 14:29:08 ; Search time 177 Seconds

(without alignments)
812.962 Million cell updates/sec

Title: US-10-077-435-1

Perfect score: 1478

Sequence: 1 MAMMEVQGGPSLGGTQVLIV.....NEHLIDMDHSAFPGAPLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: uniprot_03:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1478	100.0	281	1 TN10_HUMAN	P50591 homo sapien
2	963	65.2	287	2 O8K3GO	O8K3GO ratu mus norv
3	930	62.9	291	1 TN10_MOUSE	P50592 mus musculu
4	809.5	54.8	304	2 Q7T1F2	Q7T1F2 gallu gall
5	577.5	39.1	299	2 Q6DHG9	Q6DHG9 brachydantio
6	334.5	22.6	317	2 Q7ZYX9	Q7ZYX9 brachydantio
7	307.5	20.7	287	2 Q9DWT9	Q9DWT9 gallu gall
8	305.5	20.7	214	2 Q9DDZ5	Q9DDZ5 brachydantio
9	291	19.7	63	2 Q6TSD9	Q6TSD9 homo sapien
10	267.5	18.1	318	1 TN11_PAT	O9E8E2 r tumor nec
11	258.5	17.5	316	1 TN11_MOUSE	O35235 m tumor nec
12	251.5	17.0	317	1 TN11_HUMAN	O14788 h tumor nec
13	189.5	12.8	279	1 TNF6_MOUSE	P41047 mus musculu
14	187	12.7	280	1 TNF6_CERTO	O9BDH1 cercocebus
15	186	12.6	281	1 TNF6_HUMAN	P48823 homo sapien
16	185	12.5	280	1 TNF6_MACFA	P63308 macaca fasc
17	185	12.5	280	1 TNF6_MACMU	P63307 macaca mula
18	185	12.5	280	1 TNF6_MACNE	P63306 macaca neme
19	184.5	12.5	279	2 Q7TMV9	Q7TMV9 mus musculu
20	184	12.4	272	1 TNF5_CHICK	O918D8 gallu gall
21	182	12.3	282	1 TNF6_PIG	O9BDA8 sus scrofa
22	180	12.2	252	2 O8K3Y8	O8K3Y8 mus musculu
23	178.5	12.1	280	1 O8K1W5	O8K1W5 felis silve
24	177.5	12.0	278	1 TNF6_PAT	P36140 ratu mus norv
25	175.5	11.9	169	2 Q9WV90	Q9WV90 marmosa mon
26	175	11.8	252	2 O8K3Y7	O8K3Y7 ratu mus norv
27	173	11.7	252	2 O8K3Y7	O8K3Y7 ratu mus norv
28	166	11.2	251	2 O8NPE9	O8NPE9 homo sapien
29	164	11.1	261	1 TNF5_BOVIN	P51149 boe tauru
30	163.5	11.1	131	2 Q6J3O6	Q6J3O6 canis fami
31	160	10.8	174	1 TN15_HUMAN	O95150 homo sapien

32	159.5	10.8	240	1 TN14_HUMAN	O43557 homo sapien
33	157	10.6	154	2 O8KJ19	O8KJ19 macaca mula
34	153.5	10.4	227	2 Q7T2Q3	Q7T2Q3 cyprinu ca
35	152.5	10.3	239	1 TN14_MOUSE	O9G4H9 mus musculu
36	152	10.3	261	1 TNF5_CALTA	O9BDH3 callithrix
37	150.5	10.2	261	1 TNF5_AOTR	O9BDH3 aotus trixi
38	149.5	10.1	260	1 TNF5_FELCA	O97605 felis silve
39	149	10.1	241	2 Q6U817	Q6U817 lateolabrax
40	148	10.0	261	1 TNF5_CERTO	O6U817 cercocebus
41	148	10.0	261	1 TNF5_MACMU	P63304 macaca mula
42	147.5	10.0	260	1 TNF5_CANFA	O97626 canis fami
43	147.5	10.0	261	1 TNF5_HUMAN	P23965 homo sapien
44	144.5	9.8	216	2 Q7O332	Q7O332 mesocricetu
45	143	9.7	261	1 TNF5_PIG	O95MFS sus scrofa

ALIGNMENTS

RESULT 1
TN10_HUMAN STANDARD; PRT; 281 AA.
AC P50591;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
GN Name=TNFSF10; Synonyms=APO2L, TRAIL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713; DOI=10.1016/j.jbc.271.22.12687;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A., Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF family that induces apoptosis".
RT Immunol. 3:673-682(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96278649; PubMed=8663110; DOI=10.1074/jbc.271.22.12687;
RA Dittl R.M., Marsters S.A., Rupprecht S., Donahue C.U., Moore A., Ashkenazi A.;
RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor necrosis factor cytokine family".
RT J. Biol. Chem. 271:12687-12690(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=92388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feldgould E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D., Altshuler S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stachelson M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Urdin T.B., Toshiyuki S., Carinici P., Mullaly S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwen P.J., McKernan K.O., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W., Villalón D.K., Muzny K.C., Sodergren B.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [4]
 RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
 RX MEDLINE=200117054; PubMed=10549288; DOI=10.1016/S1097-2765(00)80207-5;
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ulicsch M., O'Connell M.,
 RA Kelley R.F., Ashkenazi A., de Vos A.M.,
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
 RT complex with death receptor 5.";
 RL Mol. Cell 4:563-571 (1999).
 [5]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
 RX PubMed=10542098; DOI=10.1038/14935;
 RA Morkoylaapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Screaton G.R.,
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 RT specificity in apoptotic initiation.";
 RL Nat. Struct. Biol. 6:1048-1053 (1999).
 [6]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
 RX MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;
 RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
 RA Sung Y.C., Oh B.-H.,
 RT "2.8 Å resolution crystal structure of human TRAIL, a cytokine with
 RT selective antitumor activity.";
 RL Immunity 11:253-261 (1999).
 CC -I- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF10E/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF10E/OPG that cannot
 CC induce apoptosis.
 CC -I- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
 CC trimer.
 CC -I- SUBUNIT: Homotrimer.
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -I- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung
 CC and prostate.
 CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC -----
 CC EMBL, U37518; AAC50332.1; -;
 DR EMBL, U57059; AAB01233.1; -;
 DR EMBL, BC037222; AAB01233.1; -;
 DR PDB, 1D0G; X-ray; A/B/D=114-281.
 DR PDB, 1D2Q; X-ray; A=114-281.
 DR PDB, 1D4V; X-ray; B=119-281.
 DR PDB, 1D66; X-ray; A=91-281.
 DR PDB, 1D03; X-ray; D/E/F/K/L=114-281.
 DR Genew; HGNC:11925; TNFSF10.
 DR H-InvDB; HIX0003863; -;
 DR MIM, 603598; -;
 DR GO, GO:0005887; C:integral to plasma membrane; TAS.
 DR GO, GO:0005625; C:soluble fraction; TAS.
 DR GO, GO:0005102; F:receptor binding; TAS.
 DR GO, GO:0007267; P:cell-cell signaling; TAS.
 DR GO, GO:0006917; P:induction of apoptosis; TAS.
 DR GO, GO:0043122; P:positive regulation of I-kappa kinase/NF-kappaB; IEA.
 DR GO, GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_1like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF_1.
 DR ProDom; PDD02012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS50049; TNF_2; 1.
 KW 3D-structure; Apoptosis; Cytokine; Metal-binding; Signal-anchor;
 KW Transmembrane; Zinc.
 FT DOMAIN 1 17 Cytoplasmic (Potential).
 FT TRANSMEM 18 38 Signal-anchor for type II membrane
 FT protein (Potential).
 FT DOMAIN 39 281 Extracellular (Potential).
 FT METAL 230 230 Zinc.
 FT STRAND 123 127
 FT STRAND 149 150
 FT STRAND 163 165
 FT STRAND 167 170
 FT STRAND 171 172
 FT TURN 173 176
 FT STRAND 180 193
 FT TURN 198 199
 FT STRAND 205 213
 FT STRAND 220 228
 FT TURN 233 234
 FT STRAND 237 250
 FT TURN 252 253
 FT STRAND 255 260
 FT HELIX 263 265
 FT STRAND 266 267
 FT TURN 270 272
 FT STRAND 274 279
 SQ SEQUENCE 281 AA; 32509 MW; DDAAE78DAAB26D CRC64;
 Query Match 100.0%; Score 1478; DB 1; Length 281;
 Best Local Similarity 100.0%; Pred. No. 4,4e-113;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGSPISGOTCVLIVFTVVLQSLCAVTVVYFTNELKQMDKYKSGIACFLYE 60
 DB 1 MAMMEVGGSPISGOTCVLIVFTVVLQSLCAVTVVYFTNELKQMDKYKSGIACFLYE 60
 QY 61 DDSYVDPNDESSMNSPCQVQVWQLRQIVRKMLIRTSEETITVQEKQONISPLVERGQ 120
 DB 61 DDSYVDPNDESSMNSPCQVQVWQLRQIVRKMLIRTSEETITVQEKQONISPLVERGQ 120
 QY 121 RVAAHITTRGRSNTLSPSNKNKEKALGRKINSWSSSGHSFSLNLRNGLVIHEKG 180
 DB 121 RVAAHITTRGRSNTLSPSNKNKEKALGRKINSWSSSGHSFSLNLRNGLVIHEKG 180
 QY 181 FYYIYSQTYFFQOEIKENTKNDKQVQYIYKTSYPPDILMKSAARNSCKDAEYGLY 240
 DB 181 FYYIYSQTYFFQOEIKENTKNDKQVQYIYKTSYPPDILMKSAARNSCKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 RESULT 2
 ID Q8K3G0 PRELIMINARY; PRT; 287 AA.
 AC Q8K3G0;
 DT 01-OCT-2002 (Tremblere). 22, Created)
 DT 01-OCT-2002 (Tremblere). 22, Last sequence update)
 DT 01-MAR-2004 (Tremblere). 26, Last annotation update)
 DE TNF-related apoptosis inducing ligand.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN NCB1_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=DA;
 RA Mueller A.M., Giegerich G.;
 RL EMBL, AY115578; AAA49797.1; -;
 DR EMBL, AY115578; AAA49797.1; -;
 DR HSSP; P50591; ID20.
 DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005164; P.tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; UNKNOWN_1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 287 AA; 32979 MW; CAAFSBBD7C833FEC CRC64;

Query Match 65.2%; Score 963; DB 2; Length 287;
Best Local Similarity 67.7%; Pred. No. 8.5e-71;
Matches 189; Conservative 29; Mismatches 51; Indels 10; Gaps 3;

QY 9 GPSLQD---TCVLVIFVTLQSLCAVATYVYFTNELKQMDKYSKSIACFLKEDSY 64
DB 9 GPSFQHFMTVITICIVLLQVLLQALTVAVTWYFNNBVKQLDNYSKIIGLACFSKEDGDF 68
QY 65 WDNDESNSSPCWQYKQRLQVLKMLRTSEBTSTQEQQNISPLVRERGPQVAA 124
DB 69 WSTDEGLINRCLQVLRQLYQLIEVTLRTPEKTIPTVEKQLSTPPLRGARRPQVAA 128
QY 125 HITGTRGSNTLSPNSKNEKALGRKINSMESSRSGHSPFLNHLRNGELVTHEKGFYI 184
DB 129 HITGTRGRNLTALIPISKQKTLGQKITWESSRSHSLNHLNGLVLYQDEGLYI 188
QY 185 VSQTYFRFQGE--EIKENTKND---KQWQYIYKTSYPPDPIILMKSARNSCMSKDAEYG 238
DB 189 VSQTYFRFKAKEASKTVSKDGRIKQWQYIYKTSYPPDPIILMKSARNSCMSREABYG 248
QY 239 LYSIYQGGIFELKENDRIFVSVTNEHLIMDHEASFGA 277
DB 249 LYSIYQGGIFELKENDRIFVSVTNEHLIMDHEASFGA 287

RESULT 3
TN10_MOUSE
ID TN10_MOUSE STANDARD; PRT; 291 AA.
AC P50592;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein).
GN Name=TNF10; Synonyms=trail;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8; Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A., Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF family that induces apoptosis";
RT that induces apoptosis";
RT Immunol 3:673-682(1995).
CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1, TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and possibly also to TNFRSF1B/OPG. Induces apoptosis. Its activity may be modulated by binding to the decoy receptors TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF1B/OPG that cannot induce apoptosis.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Widespread.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
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CC -----
DR HSBP; U37522; AAC52345.1; -
DR EMBL; P50591; ID20.
DR MGD; MGI:107414; Tnfef10.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Apoptosis; Cytokine; Signal-anchor; Transmembrane.
FT DOMAIN 1 17 Cytoplasmic (Potential).
FT TRANSMEM 18 38 Signal-anchor for type II membrane protein (Potential).
FT DOMAIN 39 291 Extracellular (Potential).
FT CARBOHYD 52 52 N-linked (GlcNAc...)(Potential).
SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 62.9%; Score 930; DB 1; Length 291;
Best Local Similarity 65.6%; Pred. No. 4.4e-68;
Matches 177; Conservative 37; Mismatches 50; Indels 6; Gaps 1;

QY 17 VLVIFVTLQSLCAVATYVYFTNELKQMDKYSKSIACFLKEDSYMDPNDESNNSP 76
DB 21 ICIVLQVLLQAVSAVATYVYFTNELKQMDKYSKSIACFLKEDSYMDPNDESNNSP 80
QY 77 CMQVQKQRLQVLRKMLRTSEBTSTQEQQNISPLVRERGPQVAAHITGRKSTLT 136
DB 81 CLQVQRQLYQLIEVTLRTPEKTIPTVEKQLSTPPLRGARRPQVAAHITGRKSTLT 140
QY 137 SSPNSKNEKALGRKINSMESSRSGHSPFLNHLRNGELVTHEKGFYIYQTYFRFQGE- 195
DB 141 LIPISKQKTLGQKITWESSRSHSLNHLNGLVLYQDEGLYIYQTYFRFQGE 200
QY 196 -----IKENTKNDKQWQYIYKTSYPPDPIILMKSARNSCMSKDAEYGLSYQGGIFEL 250
DB 201 DASKVNSDKKRTKQLQVLYIYKTSYPPDPIILMKSARNSCMSRDAEYGLSYQGGIFEL 260
QY 251 KENDRIFVSVTNEHLIMDHEASFGAPLV 280
DB 261 KENDRIFVSVTNEHLIMDHEASFGAPLV 290

RESULT 4
Q7TIF2
ID Q7TIF2 PRELIMINARY; PRT; 304 AA.
AC Q7TIF2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Tumor necrosis factor related apoptosis inducing ligand.
GN Name=TRAIL;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: Spleen;
RA Sayed A.A., Horiuchi H., Furusawa S., Matsuda H.;
RT Molecular Cloning and Characterization of Chicken Tumor Necrosis Factor (TNF)-Superfamily Ligands, CD30L and TNF-Related Apoptosis Inducing Ligand (TRAIL).
RT J. Vet. Med. Sci. 66:643-650(2004).
RL EMBL; AB114678; BAC79267.1; --

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosack S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunnarone P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maier M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC044336; AAH44336.1; -.
 DR HSSP; P50591; ID20.
 DR ZFIN; ZDB-GENE-010801-1; tngef101.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS50049; TNF 2; 1.
 SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DC9F CRC64;

Query Match 22.6%; Score 334.5; DB 2; Length 317;
 Best Local Similarity 29.2%; Pred. No. 3.7e-19;
 Matches 83; Conservative 55; Mismatches 113; Indels 33; Gaps 8;

QY 18 LIVITFTVLQSLCVAVTVYVFTNELKQMDKXSKSGIACF-----LKEEDSDVMDPD-BE 71
 Db 40 MWIVVVVVLQIASVTGLFVYLNMSLSQVQGTBEELRLGLNLVGLKQODI--PEDLQ 97
 QY 72 SNNSPCWQVQWQLRQLVRKM-----LRTSEETISTVOEKQNISPLVERGCP 120
 Db 98 LFGECEMKLAEIGIKAYISKVTSIISKOTLHAARTHTTSGSFMTTV-----NQ 150
 QY 121 RVAHAHITGRGSRNT-----LSSPNSKNEKALGRKINSWESSRGHSFLSNLHNGELV 175
 Db 151 RPSAHLTLSSASDNSRPGSDMHQPOFDLHQSCHRPVHTW-ANKSFGAHLNNMTLTGRLR 209
 QY 176 IHEKEFYIYSQTYRFR-QBEIKENTKNDKQWQYIYKTSYDPDLLMKSNRNSQSKMD 234
 Db 210 VPQDRYIYISQVYRFPSPSDSDSSVSHQLVQCCTYKKTSTYLNPIQLKGVGTCKWAPD 269
 QY 235 AEYGLYSIYQGIIFELKENDRIFVSVTNEHLIDMDHEASFGAF 278
 Db 270 AEYALHSYQGLFELKADDEVFVSISPTMYGSESSYFGAF 313

RESULT 7
 Q9DWT9 PRELIMINARY; PRT; 287 AA.
 AC Q9DWT9;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DR TNF-related apoptosis inducing ligand-like protein.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Briggham J.T., Johnson A.L.,
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY057941; AAL23702.1; -.
 DR HSSP; P50591; ID20.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR Pfam; PF00229; TNF; 1.
 DR PROSITE; PS002012; TNF_subf; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS50049; TNF 2; 1.
 SQ SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;

Query Match 20.8%; Score 307.5; DB 2; Length 287;
 Best Local Similarity 32.3%; Pred. No. 5.3e-17;
 Matches 93; Conservative 46; Mismatches 110; Indels 39; Gaps 11;

QY 18 LIVITFTVLQSLCVAVTVYVFT-----NELKQMDKXSKSGIACFLKEDSDYWD 66
 Db 8 LHAFTSLLEQLPLCTAPEMAGTWSQALQNAFRLKQSGSSBELRLCLQLNQDQEG 67
 QY 67 PNDESM-NSPCWQVQWQLRQLVRKMILRTSEET--STVOEKQ--NISF-LVREKCP 119
 Db 68 SNLEELISNQC-----LKLANTIKAYVATVTEENVISRSVNEAKSYFNISGOVATKTL 123
 QY 120 QVVAHI-----TGRGSRNTLSSPNSKNEKALGRKINSWESSRGHSFLSNLHLR 170
 Db 124 GKPSAHLIFRPQNPADQSSRFNGLS-----QSCRHAIRWEDS-TISHLQNIYTR 175
 QY 171 NGEIYIHEKEFYIYSQTYRFRQBEIKENTKNDKQWQYIYKTSYDPDLLMKSNRNSC 230
 Db 176 DGRILNVNQAGKYYVVSQIYFRYSRDGAGARVSPVLVQCINMKTSYSGQITLLKGVGTIC 235
 QY 231 WSKDAEYGLYSIYQGIIFELKENDRIFVSVTNEHLIDMDHEASFGAF 278
 Db 236 WAPAEYGLHALYQGLFELKAGDELFFVSSLAIDYSDAASYPGAF 283

RESULT 8
 Q9DD25 PRELIMINARY; PRT; 214 AA.
 AC Q9DD25;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE TRAIL-like protein.
 GN Name=tnfsf101;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bobe J., Goetz F.W.,
 RT "Molecular cloning and expression of a TNF receptor and two TNF
 RT ligands in the fish ovary.";
 RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481 (2001).
 DR EMBL; AF250041; AAG47640.1; -.
 DR HSSP; P50591; ID20.
 DR ZFIN; ZDB-GENE-010801-1; tnfsf101.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS50049; TNF 2; 1.
 SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

Query Match	Similarity	20.7%	Score 305.5	DB 2	Length 214
Best Local	Similarity 37.6%	Pred. No. 5.3e-17			
Matches	62	Conservative 37	Mismatches 59	Indels 7	Gaps 3
Qy	120	QVAAHITGTGRSNT-----LSSPNSKNEKALGRKINSWESSRSGHSLNLRLNGL	174		
Db	47	QRPAAHLTLSSADNSRSPQSDMHQPFQDLHGSCHRPVHTW-ANKSFGAHLVMTLTNRL	105		
Qy	175	VIHKGFFYYITSQYFRF-QSEIKENTKNDQMOYIYIKTYSYPPILMKSARNSCMK	233		
Db	106	RVPDDGRYYLTSQYFRFSPSSDSSQSSVSHQVQCIYKTKTNSYLPIDLKGVTGWAP	165		
Qy	234	DAEYVLSIYOGGIFELKFNENRIFVSYNEHLIMDHDEASFGAP	278		
Db	166	DAEYVLSIYOGGIFELKFNENRIFVSYNEHLIMDHDEASFGAP	210		
RESULT 9					
Q6JSD9		PRELIMINARY:	PRT:	63 AA.	
AC	Q6JSD9				
DT	05-JUL-2004	(TREMBLrel. 27, Created)			
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)			
DE		Chemokine tumor necrosis factor ligand superfamily member 10 (Fragment).			
GN		Name=TNFSF10;			
OC		Homo sapiens (Human).			
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC		Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
NCBI		_TaxID=9606;			
RL		SEQUENCE FROM N.A.			
RC		Tissue=Lung carcinoma;			
RA		Poivi A., Ruusaari S., Vendelin J., West A., Saarikko I.,			
RA		Reinikainen A., Hollmen J., Laitinen T., Mannila H., Lahtesmaa R.,			
RA		Kere J.;			
RL		Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
DR		EMBL; AY132579; AAR16184.1; --			
SO		NON TER			
SO		SEQUENCE 63 AA; 7638 MW; 8F0C7936DA5A5A6E6 CRC64;			
Query Match		19.7%	Score 291;	DB 2;	Length 63;
Best Local		Similarity 100.0%	Pred. No. 1.7e-16;		
Matches	52	Conservative 0	Mismatches 0;	Indels 0;	Gaps 0;
Qy	39	TNELKQMDKTKSKGIAFLKEDDSYMPNDPNEBSNNSGCMQYKQRLQRLVRK	90		
Db	1	TNELKQMDKTKSKGIAFLKEDDSYMPNDPNEBSNNSGCMQYKQRLQRLVRK	52		
RESULT 10					
TN1L_RAT		STANDARD:	PRT:	318 AA.	
ID	TN1L_RAT				
AC	Q9SE22; G91Z19;				
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	05-JUL-2004	(Rel. 44, Last annotation update)			
DE		Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF).			
GN		Name=Trnfsl1; Synonyms=Opgl; Rankl; Trance;			
OC		Rattus norvegicus (Rat).			
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC		Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.			
NCBI		_TaxID=10116;			
RL		SEQUENCE FROM N.A.			
RC		Tissue=Tibial bone;			
RC		MEDLINE=20540945; PubMed=11092396;			
RA		Xu J.-K., Tan J.-K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,			

RA	Zheng M.H.;
RT	"Cloning, sequence and functional characterization of the rat
RT	homologue of receptor activator of NF- κ B ligand.";
RL	J. Bone Miner. Res. 15:2178-2186(2000).
RN	[2]
RP	SEQUENCE OF 266-318 FROM N.A.
RC	STRAIN=Fischer 344;
RX	MEDLINE=21662371; PubMed=11804028;
RA	Ogden P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savas A.,
RA	Satadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
RA	Marks S.C. Jr.;
RT	"Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT	the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene";
RL	Int. J. Dev. Biol. 45:853-859(2001)
CC	-I- FUNCTION: Cytokine that binds to TNFRSF11B/ODG and to
CC	TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC	Augments the ability of dendritic cells to stimulate naive T-cell
CC	proliferation. May be an important regulator of interactions
CC	between T cells and dendritic cells and may play a role in the
CC	regulation of the T cell-dependent immune response. May also play
CC	an important role in enhanced bone-reabsorption in humoral
CC	hypercalcaemia of malignancy.
CC	-I- SUBUNIT: Homotrimer (By similarity).
CC	-I- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC	similarity).
CC	-I- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
CC	-I- PFM: The soluble form derives from the membrane form by
CC	proteolytic processing (By similarity).
CC	-I- SIMILARITY: Belongs to the tumor necrosis factor family.
CC	-----
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CC	or send an email to license@sib-sib.ch).
CC	-----
DR	EMBL, AF187319, AAC17031.1; -.
DR	EMBL, AF425669, AAL23963.1; -.
DR	HSSP, O35235, IUTZ.
DR	RCD, G20784, Tntef11.
DR	InterPro: IPR006052; TNF family.
DR	InterPro: IPR008983; TNF_like
DR	InterPro: IPR003636; TNF_subf.
DR	Pfam, PF00229; TNF; 1.
DR	ProDom: PD002012; TNF_subf; 1.
DR	SMART: SM00207; TNF; 1.
DR	PROSITE, PS00251; TNF_1; FALSE_NEG.
DR	PROSITE, PS50049; TNF_2; 1.
KW	Cytokine; Differentiation; Glycoprotein; Receptor; Signal-anchor;
KW	Transmembrane.
FT	CHAIN 1 318
FT	CHAIN 141 318
FT	DOMAIN 1 47
FT	TRANSMEM 48 68
FT	DOMAIN 69 318
FT	SITE 140 141
FT	CARBHYD 199 199
FT	CARBHYD 264 264
FT	CONFLICT 317 317
SO	SEQUENCES 318 AA; 35370 MW; 4B874AD706AD098F CRC64;
QY	Query Match 18.1%; Score 267.5; DB 1; Length 318;
	Best Local Similarity 27.3%; Pred. No. 1.2e-13;
	Matches 82; Conservative 55; Mismatches 106; Indels 57; Gaps 11;
D0	10 PSLGQTCLVIFVTLLQSICAVNTYYYFNTELKOMDKYSKGIACF-----LKED--- 61
	43 PAASRFMLDLGIGAGQVCSTALFYFAQMD--PNRISBSDBSTRCTFYILRLRKRENTGL 100

OY 62 -DSYWDPNDESMNSPCMOVKQLRQVLRKMLRTSEETSTVOEKOQNSPLVERGPO 120
 DB 101 QDSTLESEDTXALPDSRCRMKAFO-----GAVORELOHV-----GPO 139
 OY 121 R---VAAHITGT-----RGRS-----NTLSPNSKNEKALGRKINSMESRSGH 161
 DB 140 RSSGVPAMMESGWLVARRGKEAPFALHTINADIPESGKVL-----SSWYHDR-CW 194
 OY 162 SFLSNLHLRNGELVHKEGFYIYSQTYFRQOEIKENTKDKQNVQIYKYT-SYDPDI 220
 DB 195 AKISNWTLSNGKLRVNOQDFYLLVYANICFRHHETSGSVADYLDQLMVYVVKTSIKIPSSH 254
 OY 221 LLMKARSCKSKDKEVGLGYSIYOGGIFELKENDRIPVSYTMELHLDMDHESFPGAFV 280
 DB 255 NLMKSGTKMWSGNSSEFHFYSINVGGFFLARGEEISVQVSNPSLDDPDQDYTFGAFV 314
 RESULT 11
 TN11_MOUSE STANDARD; PRT; 316 AA.
 AC 035235; 035306; 09JUK8; 09JUK9; 09RIY0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
 differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
 (OCIF).
 DE (OCIF).
 GN Name=Trsf11; Synonyms=OPGL, RANKL, Trance;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hybridoma; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
 RA MEDLINE=97460112; PubMed=97460112; Robinson E., Orlinick J., Chao M.,
 RA Wong B.R., Rho J., Aron J., Robinson E., Orlinick J., Chao M.,
 RA Kalachikov S., Cayan E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RA "TRANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells.";
 RL J. Biol. Chem. 272:25190-25194(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thymic lymphoma; PubMed=9367155; DOI=10.1038/36593;
 RA MEDLINE=98032977; PubMed=9367155; Billingsley W.L., Dougal W.C.,
 RA Anderson D.M., Warrakovsky E., Billingsley W.L., Dougal W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Gaibero L.;
 RA "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
 RA MEDLINE=98227661; PubMed=9568710; Tan H.-L., Kelley M.J., Dunstan C.R.,
 RA Lacey D.L., Timme E., Tan H.-L., Kelley M.J., Dunstan C.R.,
 RA Burgess T., Elliott R., Colombero A., Elliott C., Scully S., Hsu H.,
 RA Sullivan J., Hawkins N., Davy B., Capparello C., Eli A., Qian Y.-X.,
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
 RA Boyle W.J.;
 RA "Osteoprotegerin ligand is a cytokine that regulates osteoclast
 RT differentiation and activation.";
 RL Cell 93:165-176(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow stroma; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
 RA MEDLINE=98188248; PubMed=9520411; Yamaguchi K., Kinoshita M.,
 RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M.,
 RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,

RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
 RT "Osteoclast differentiation factor is a ligand for
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
 RT to TRANCE/RANKL.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=129;
 RA MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
 RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
 RA Ueda M., Higashio K.;
 RT "Cloning and characterization of the gene encoding mouse osteoclast
 RT differentiation factor.";
 RL Gene 230:121-127(1999).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RA MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
 RT "Determination of three isoforms of the receptor activator of nuclear
 RT factor-kappaB ligand and their differential expression in bone and
 RT thymus.";
 RL Endocrinology 142:1419-1426(2001).
 RN [7]
 RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
 RA MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
 RA Lum L., Wong B.R., Jost R., Becherer J.D., Erdjument-Bromage H.,
 RA Schindler J., Tempst P., Choi Y., Blobel C.P.;
 RT "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
 RT converting enzyme-like protease in shedding of TRANCE, a TNF family
 RT member involved in osteoclastogenesis and dendritic cell survival.";
 RL J. Biol. Chem. 274:13613-13616(1999).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
 RA MEDLINE=21464816; PubMed=11581298;
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
 RT of receptor-ligand specificity.";
 RL J. Clin. Invest. 108:971-979(2001).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
 RA MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200;
 RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at
 RT 2.2-A resolution.";
 RL J. Biol. Chem. 277:6631-6636(2002).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcaemia of malignancy.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O35235-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O35235-2; Sequence=VSP_006449;
 CC Name=3;
 CC IsoId=O35235-3; Sequence=VSP_006448;
 CC -1- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
 CC but not in nonlymphoid tissues and is abundantly expressed in T
 CC cells but not in B cells. A high level expression is also seen in
 CC the trabecular bone and lung.
 CC -1- PTM: N-glycosylated.
 CC -1- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing. The cleavage may be catalyzed by
 CC ADAM17. A further shorter soluble form was observed.
 CC -1- DISEASE: Deficiency in Trsf11 results in failure to form lobulo-

CC alveolar mammary structures during pregnancy, resulting in death
 CC of newborns. Trance-deficient mice show severe osteopetrosis, with
 CC no osteoclasts, marrow spaces, or tooth eruption, and exhibit
 CC profound growth retardation at several skeletal sites, including
 CC the limbs, skull, and vertebrae and have marked chondrocytasia,
 CC with thick, irregular growth plates and a relative increase in
 CC hypertrophic chondrocytes.
 CC
 CC -1 SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC -----
 CC EMBL; AF013170; AAC71061.1; -
 CC EMBL; AF013048; AAB86812.1; -
 CC EMBL; AF053713; AAC40113.1; -
 CC EMBL; AB008426; BAA25425.1; -
 CC EMBL; AB022039; BAA36970.1; -
 CC EMBL; AB022037; BAA36970.1; JOINED.
 CC EMBL; AB022038; BAA36970.1; JOINED.
 CC EMBL; AB032772; BAA97257.1; -
 CC EMBL; AB032772; BAA97258.1; -
 CC EMBL; AB036798; BAA97259.1; -
 CC PDB; 1IOA; X-ray; A/B/C-157-316.
 CC PDB; 1UTZ; X-ray; X/Y/2-146-316.
 CC WGD; MG1; 1100089; Tntf11.
 CC DR GO; GO:000515; F:protein binding; IPI.
 CC DR GO; GO:0042804; P:protein homooligomerization activity; IDA.
 CC DR GO; GO:0045453; P:bone resorption; IDA.
 CC DR GO; GO:0009887; P:osteogenesis; IMP.
 CC DR GO; GO:0001503; P:osteification; IMP.
 CC DR InterPro; IPR006052; TNF family.
 CC DR InterPro; IPR008983; TNF like.
 CC DR InterPro; IPR003636; TNF_subf.
 CC DR Pfam; PF00229; TNF; 1.
 CC DR ProDom; PD002012; TNF_subf; 1.
 CC DR SMART; SM00207; TNF; 1.
 CC DR PROSITE; PS00251; TNF_1; FALSE_NEG.
 CC DR PROSITE; PS50049; TNF_2; 1.
 CC DR 3D-structure; Alternative splicing; Cytokine; Differentiation;
 CC Direct protein sequencing; Glycoprotein; Receptor; Signal-anchor;
 CC Transmembrane.
 CC FT CHAIN 1 316 Tumor necrosis factor ligand superfamily
 CC FT CHAIN 139 316 member 11, membrane form.
 CC FT DOMAIN 1 48 Tumor necrosis factor ligand superfamily
 CC FT TRANSMEM 49 69 member 11, soluble form.
 CC FT CYTOPLASMIC (Potential).
 CC FT SIGNAL-ANCHOR (Potential).
 CC FT SIGNAL-ANCHOR FOR TYPE II membrane
 CC FT PROTEIN (Potential).
 CC FT EXTRACELLULAR (Potential).
 CC FT CLEAVEAGE.
 CC FT SITE 138 139 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 197 199 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 262 262 Missing (in isoform 3).
 CC FT VARSPPLIC 1 117 /FTIdVSP 006448.
 CC FT VARSPPLIC 14 44 SSBEMSGSPGVPHBGLHAPAPAPAPPPA -> TP (in
 CC FT VARSPPLIC 14 44 isoform 2).
 CC FT CONFLICT 99 99 /FTIdVSP 006449.
 CC FT CONFLICT 141 143 G -> D (in Ref. 2).
 CC FT STRAND 164 169 Missing (in Ref. 5).
 CC FT TURN 171 172
 CC FT STRAND 181 182
 CC FT STRAND 186 187
 CC FT TURN 191 192
 CC FT STRAND 194 196
 CC FT STRAND 198 201

FT TURN 202 203
 Query Match 17.5%; Score 258.5; DB 1; Length 316;
 Best Local Similarity 26.4%; Pred. No. 6.3e-13;
 Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
 QY 10 PSLGCTCYLIVFYVLLSLCAVATVYVFTNELKOMDKYKSGIAC-----LKEDSY 64
 DB 43 PAASRSMFLALIGLGLGVVCSIALFLYFRQMD--PFRISEDTHCYRILRLHENG 100
 QY 65 MDP--NDESNSSPCOWKQQLRQLVRKMLRTSETISTYOEKOONISPL----- 113
 DB 101 QDSTLSESDTLPDSCTRRKQAFQAVQK-----ELQHYVFPQFSAPAMM 146
 QY 114 -----VERGFORVA--AHITGRGNTLSPNSKNEKALGRKINSMESSRSGHFLS 165
 DB 147 EGSWLDVAQRGKEAPQPAHLT-----INAAISPGSHKVTL---SSWYHDR-GMAKIS 196
 QY 166 NMLRNGELVTHKEGFYITIGQTFRRFOEIKENTKDKQVQIYKKT-SYPPDILMK 224
 DB 197 NMTLSNGRLRVQDGFYLYANICFRHETSGSVPTDYLQMVVYVYKTSIKIPSSHNLMK 256
 QY 225 SARNSCWKDAEYGLYSYVGIGIFELKENDRIFVSTNEHLIDMDHEASFGAFLV 280
 DB 257 GGSTKMSGNSBFRFYSINVGAFKLRAGEISIQVSNPSLDDPDQATYFGAFKV 312
 RESULT 12
 ID TN11_HUMAN STANDARD; PRT; 317 AA.
 AC 014788; 014723; 096017; 09P203;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
 DE differentiation factor) (ODF).
 GN Name=TNFSF11; Synonyms=OPGL, RANKL, TRANCE;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow, and Peripheral blood;
 RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougan W.C.,
 RA Tometsko W.E., Roux B.R., Teepe W.C., Duboe R.F., Coeman D.,
 RA Galibert L.;
 RA "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RA and dendritic-cell function.";
 RA Nature 390:175-179 (1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lymph node;
 RX MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
 RA Lacey D.L., Timme B., Tan H.-L., Kelley M.J., Duncan C.R.,
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hu H.,
 RA Sullivan D., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
 RA Kautman S., Sarosi I., Shalhoub V., Senaldi G., Guo D., Delaney J.,
 RA Boyle W.J.;
 RA "Osteoprotegerin ligand is a cytokine that regulates osteoclast
 RA differentiation and activation.";
 RA Cell 93:165-176 (1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RA Ikeda T., Kuroyama H., Hirokawa K.;
 RA "Determination of human RANKL isoforms.";
 RA Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 73-317 FROM N.A.
 RC TISSUE=Thymocytes;

RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
 RA Wong B.R., Rho J., Aron J., Robinson E., Orlinkick J., Chao M.,
 RA Kalachikov S., Cayan E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.,
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates C-Jun N-terminal kinase in T cells.";
 RL J. Biol. Chem. 272:25190-25194(1997).
 RN [5].
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Tongue;
 RX MEDLINE=20175237; PubMed=10708588; DOI=10.1006/brc.2000.2314;
 RA Nagai M., Kyakumoto S., Sato N.,
 RT "Cancer cells responsible for humoral hypercalcemia express mRNA
 RT encoding a secreted form of ODF/TRANCE that induces osteoclast
 RT formation.";
 RL Biochem. Biophys. Res. Commun. 269:533-536(2000).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
 CC secreted (isoform 2). A soluble form of isoform 1 arises by
 CC proteolytic processing (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O14788-1; Sequence=Displayed;
 CC Name=2; Synonyms=SOBF;
 CC IsoId=O14788-2; Sequence=VSP_006447;
 CC Name=3;
 CC IsoId=O14788-3; Sequence=VSP_006446;
 CC -1- TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
 CC spleen, peripheral blood leukocytes, bone marrow, heart, placenta,
 CC skeletal muscle, stomach and thyroid.
 CC -1- INDUCTION: Up-regulated by T cell receptor stimulation.
 CC -1- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing (By similarity). The cleavage may be
 CC catalyzed by ADAM17.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC -----
 CC EMBL; AF019047; AAB86811.1; -
 CC EMBL; AF053712; AAC39731.1; -
 CC EMBL; AB064263; BAB79694.1; -
 CC EMBL; AB061227; BAB71768.1; -
 CC EMBL; AB064270; BAB79695.1; -
 CC EMBL; AF013171; AAC51762.1; -
 CC EMBL; AB037599; BAA90488.1; -
 CC HSSP; O35235; LJTZ.
 CC Genew; HGNC:11926; TNFRSF11.
 CC MIM; 602642; -
 CC GO; GO:0005576; C:extracellular; NAS.
 CC GO; GO:0005887; C:integral to plasma membrane; NAS.
 CC GO; GO:0005164; P:tumor necrosis factor receptor binding; NAS.
 CC GO; GO:0006955; P:immune response; NAS.
 CC GO; GO:0030316; P:osteoclast differentiation; NAS.
 CC InterPro; IPR006052; TNF_family.
 CC InterPro; IPR008983; TNF_like.
 CC Pfam; PF00229; TNF_1.
 CC ProDom; PD002012; TNF_subf; 1.

DR SMART; SMO0207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; FALSE_NEG.
 DR PROSITE; PS50049; TNF_2; 1.
 KW Alternative splicing; Cytokine; Differentiation; Glycoprotein;
 KW Receptor; Signal-anchor; Transmembrane.
 FT CHAIN 1 317 Tumor necrosis factor ligand superfamily
 FT member 11, membrane form.
 FT CHAIN 140 317 Tumor necrosis factor ligand superfamily
 FT member 11, soluble form (By similarity).
 FT DOMAIN 1 47 Cytoplasmic (Potential).
 FT TRANSMEM 48 68 Signal-anchor for type II membrane
 FT protein (Potential).
 FT DOMAIN 69 317 Extracellular (Potential).
 FT SITE 139 140 Cleavage (By similarity).
 FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 198 198 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 1 47 Missing (in isoform 3).
 FT VARSPLIC 1 73 Missing (in isoform 2).
 FT VARSPLIC 1 73 Missing (in isoform 2).
 FT CONFLICT 194 194 A -> G (in Ref. 4).
 FT SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;
 SO SEQUENCE
 Query Match 17.0%; Score 251.5; DB 1; Length 317;
 Best Local Similarity 24.1%; Pred. No. 2.4e-12;
 Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;
 QY 10 PSLGQTCVLIIVFTYLLSLCYAVTYVTFNELKQMDKYSAGIACF-----LKED--- 61
 DB 42 PAASRSMFVALGLGLGVVCSVALFFYFRQMD--PRISBDGTHCIYRIURHENDP 99
 QY 62 -DSYNDPNDDESMNSPCQVQK-----QLROLVRRKMLITTSBETI-----STVQEQ 107
 DB 100 QDTLESQPTKLIIPSCRIKQAFQGAQVQKELQHVSGCHIIAERAMVDGSLDAKSK 159
 QY 108 QNISPLVERGEPQVRAAHITGRGRSNTLSSPNSKREKALGRKINSWESSRSGHPLSNTL 167
 DB 160 LEAGF-----AHLT-----INATDIPSGHXYSL-----SWVHDR-GMAKISGM 199
 QY 168 HLRNGELVIERKGPYYITSQYFRQOEIKENTKDKQMVQIYYT-STYDPIILMKSA 226
 DB 200 TFSNGKLIYNQDGFYLLVLANICFRHETSGDATEYLDLMVYVYTSIKIPSSHTLMKGG 259
 QY 227 RNSCKSAEVLGYSIYGGIFELKENDRIPVSVNHEILMDHSAFPGALV 280
 DB 260 STKWSGSEFHFYSINVGFFKLNSGGEISIEVSNPSULDPDQATYFGAKV 313
 RESULT 13
 TNF_MOUSE STANDARD; PRT; 279 AA.
 ID TNF_MOUSE
 AC P41047; Q61217; Q9RIE2;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
 DE ligand).
 GN Name=TNFsf6; Synonyms=APTL1G1, Fasl, gld;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RX MEDLINE=94185175; PubMed=7511063; DOI=10.1016/0092-8674(94)90375-1;
 RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
 RA Suda T., Nagata S.,
 RT "Generalized lymphoproliferative disease in mice, caused by a point
 RT mutation in the Fas ligand.";
 RL Cell 76:969-976(1994).
 RN (2)
 RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
 RC STRAIN=C57BL/6;

RX MEDLINE=9538076; PubMed=7544870; DOI=10.1016/0161-5890(95)00016-8;
 RA Peltsch M.J., Tschopp J.J.;
 CC "Comparative molecular modelling of the Fas-ligand and other members
 RT of the TNF family.";
 RL Mol. Immunol. 32:761-772(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RX MEDLINE=95196085; PubMed=7889405; DOI=10.1016/1074-7613(94)90106-6;
 RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
 RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
 RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a TNF
 RT family gene cluster.";
 RL Immunity 1:131-136(1994).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RX STRAIN=BALB/c;
 RA Fenner M.H., Shioda T., Issebacher K.J.;
 RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in two
 RT amino acids.";
 RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RX STRAIN=C3H; TISSUE=Spleen;
 RA MEDLINE=20021694; PubMed=10552956;
 RA Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,
 RA Cananale L., Migliorati G., Delfino D.V., Riccardi C.;
 RT "Cloning and expression of a short Fas ligand: a new alternatively
 RT spliced product of the mouse Fas ligand gene.";
 RL Blood 94:3456-3467(1999).
 RN [6]
 RP CHARACTERIZATION OF VARIANT GLD.
 RX MEDLINE=96091792; PubMed=7495745;
 RA Hahne M., Peitsch M.C., Imtler M., Schroeter M., Lowin B.,
 RA Roussseau M., Bron C., Renno T., French L., Tschopp J.;
 RT "Characterization of the non-functional Fas ligand of gld mice.";
 RL Int. Immunol. 7:1381-1386(1995).
 RN [7]
 RP VARIANTS ALA-184 AND GLY-218.
 RX STRAIN=BALB/c, C3H, C57BL/6, DBA/1, DBA/2, MRL, NOD, NZB, NZW, and
 RC SJL;
 RA MEDLINE=97268671; PubMed=9108079; DOI=10.1073/pnas.94.8.3914;
 RA Kagasaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,
 RA Yagita H.;
 RT "Polymorphism of murine Fas ligand that affects the biological
 RT activity.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).
 RN [8]
 RP FUNCTION: Cytokine that binds to TNFRSF6/Fas, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/Fas-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance. In the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/Dcr3
 CC modulates its effects (by similarity).
 CC [9]
 RP SUBUNIT: Homotrimer (Probable).
 CC [10]
 RP SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
 CC Secreted (isoforms FASL and FASLS).
 CC [11]
 RP ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=FasL;
 CC IsoId=P41047-1; Sequence=Displayed;
 CC Name=FASLS;
 CC IsoId=P41047-2; Sequence=VSP_006445;
 CC [12]
 RP PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC [13]
 RP DISEASE: A deficiency in this protein (gld) is the cause of generalized
 CC lymphoproliferation disease phenotype (gld). Gld mice present
 CC lymphadenopathy and autoantibody production. The phenotype is
 CC recessively inherited.
 CC [14]
 RP SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC -----

CC EMBL, U06948; AAA17800.1; -
 DR EMBL, U10984; AAA19778.1; -
 DR EMBL, S76752; AAB33780.1; -
 DR EMBL, U58995; AAB02915.1; -
 DR EMBL, AF19335; AAD52106.1; -
 DR PIR, A53062; A53062.
 DR HSBP, P50581; 1D66.
 DR MGD; MG1:99255; Tnfaf6.
 DR InterPro; IPR008064; Fas_ligand.
 DR InterPro; IPR006053; TNF_abc.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF_1.
 DR PRINTS; PR01681; FASLIGAND.
 DR PRODOM; PD002012; TNF_subf.1.
 DR PROSITE; PS00251; TNF_1.1.
 DR PROSITE; PS00049; TNF_2.1.
 KW Alternative splicing; Apoptosis; Disease mutation;
 KW Glycoprotein; Polymorphism; Signal-anchor; Transmembrane.
 FT CHAIN 1 279
 FT
 FT CHAIN 128 279
 FT
 FT DOMAIN 1 78
 FT TRANSMEM 79 100
 FT
 FT DOMAIN 101 279
 FT
 FT DOMAIN 4 69
 FT SITE 127 128
 FT DISULFID 200 231
 FT CARBOHYD 117 117
 FT CARBOHYD 182 182
 FT CARBOHYD 248 248
 FT CARBOHYD 258 258
 FT VARSPLIC 1 210
 FT
 FT VARIANT 184 184
 FT
 FT VARIANT 218 218
 FT
 FT VARIANT 273 273
 FT
 SQ SEQUENCE 279 AA; 31442 MW; 3797282728E0A1CA CRC64;
 Query Match 12.8%; Score 189.5; DB 1; Length 279;
 Best Local Similarity 25.8%; Pred. No. 2.5e-07;
 Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;
 QY 83 QLRQLVRKMLRTSETISITVOEKQONISPIVREKGPQVAAHITGSRSTLSPSPSK 142
 DB 111 ELREFTNOSL-----KISSPEKQIANPSTSEKKEPSSV-AHLTG-----NPISR 154
 QY 143 NEKALGRKINSWESSRSGHSPLSNLHLRNGELVIHEKGFYYISQTYRRPOEIKENTKN 202
 DB 155 SLPL-----EWEDF-YGVALLISGVKKYKGGVLINETGLVYFYSKYFRGQ-----SCN 201
 QY 203 DKQWQVIY-KYTSPPDILMKSR-NSCMSKDAEGLYSYOGIEFLKNDRIFFSV 260
 DB 202 NQPLNHKKYMYRNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGAIVNLTSADHLVYNI 259
 QY 261 TNEHLIDMDEASPRGAF 278
 DB 260 SOLSLINFEESKTFPGLY 277

RESULT 14
 TNF6 CERTO STANDARD: PRT: 280 AA.
 AC Q9BDN1
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand) (CD95L protein).
 GN Name=TNFRSF6; Synonyms=CD95L, FASL.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Cercopithecus.
 NC NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=21381618; PubMed=11491535; DOI=10.1007/s002510100322;
 RA Villinger F., Boeslik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate Fae/Fas ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects (By similarity).
 CC -1- SUBUNIT: Homotrimer (Probable).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).
 CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
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 CC -----
 CC EMBL: AF344847; AK37606.1; -.
 DR HSSP: P50591; 1DQ.
 DR InterPro: IPR008064; Fae ligand.
 DR InterPro: IPR006053; TNF_abc.
 DR InterPro: IPR006052; TNF_family.
 DR InterPro: IPR008983; TNF_like.
 DR InterPro: IPR003636; TNF_subf.
 DR Pfam: PF00229; TNF_1.
 DR PRINTS: PR01681; FASLIGAND.
 DR PRINTS: PR01234; TNFCROSISCT.
 DR PRODOM: PP002012; TNF_subf; 1.
 DR SMART: SM00207; TNF_1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 KW Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
 FT CHAIN 1 280 Tumor necrosis factor ligand superfamily member 6, membrane form.
 FT CHAIN 129 280 Tumor necrosis factor ligand superfamily member 6, membrane form.
 FT DOMAIN 1 80 Cytoleamic (Potential).
 FT TRANSMEM 81 101 Signal-anchor for type II membrane protein (Potential).
 FT DOMAIN 102 280 Extracellular (Potential).
 FT DOMAIN 4 69 Pro-rich.
 FT DOMAIN 45 64 Poly-Pro.
 FT SITE 128 129 Cleavage (By similarity).
 FT DISULFID 201 232 Potential.

FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 249 249 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 259 259 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 280 AA; 31407 MW; 729EA6067BD398 CRC64;
 Query Match 12.7%; Score 187; DB 1; Length 280;
 Best Local Similarity 22.1%; Pred. No. 4e-07;
 Matches 61; Conservative 56; Mismatches 91; Indels 68; Gaps 10;
 QY 4 MEVGGSPSLGQTCVIVIFVTLQSLCVAIVYVYFTNLKQMDKYSKGIACFLKEDS 63
 DB 70 LKKRNHSTG-LCLLMFPMVLVALVGGLMFOFLHOKELAE-----LRSTSS 118
 QY 64 YWPDDESNMSPCMQVQKQLRQLVRKMLIRTSSEITISVQKQNIISPLVERGPQVVA 123
 DB 119 -----QKTHASLKLQIQHPSP-PEKKEQRKV 145
 QY 124 AHITGRGRSNTLSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVIEKGFY 183
 DB 146 AHLTG-----KPNRSMPPL-----EWEDT-YGIVLISGVYKKGGLVINEYGLYF 189
 QY 184 IYSQYFRFQREIKENTKNDKQMYIY-KTYSYDPILMKSNRNSCMSDAEYGLSI 242
 DB 190 VYSKYVFRGQ-----SCTNLPLSHKYVYRNSKYPQDLVMEGRKMS-YCTTGQMMHSS 242
 QY 243 YQGIFELKENDRIFVSYTNEHLIDMDHEASFFGAF 278
 DB 243 YLGAVFNLSTDLHYLVNSELVNFESQTFPGLY 278
 RESULT 15
 TNF6 HUMAN STANDARD: PRT: 281 AA.
 ID TNF6_HUMAN
 AC P48023; Q9BZP9;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand) (Apoptosis antigen ligand) (APTL) (CD178 antigen).
 GN Name=TNFRSF6; Synonyms=APTL1G1, FASL;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=95105731; PubMed=7528780;
 RA Alderson M.;
 RT "Fas ligand mediates activation-induced cell death in human T lymphocytes".
 RL J. Exp. Med. 181:71-77(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=95127560; PubMed=7826947;
 RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
 RT "Human Fas ligand: gene structure, chromosomal location and species specificity".
 RL Int. Immunol. 6:1567-1574(1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Schaeuble C.E., Poehmann R., Philippen P., Eidel H.;
 RL Submitted (JUN-1995) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=95071350; PubMed=780502;
 RA Mita E., Hayashi N., Ito S., Takehara T., Hijioka T., Kasehara A.,
 RA Fusumoto H., Kamada T.;
 RT "Role of Fas ligand in apoptosis induced by hepatitis C virus infection".
 RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Leukocyte;

RA Zeylun A., Nagarkatti M., Nagarkatti P.S.:
 RT "Isolation and characterization of a new naturally occurring variant of
 human Fas ligand that is expressed only in membrane bound form.",
 RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Wilkinson J.:
 RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Blood;
 RX MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klansner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE-Blood;
 RA Matsumura M., Nakanishi Y., Ohba Y.:
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
 RX MEDLINE=97373583; PubMed=9228058; DOI=10.1074/jbc.272.30.18827;
 RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi F.,
 RA Teschke A., Peitsch M.C., Tschopp J.:
 RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
 RL J. Biol. Chem. 272:18827-18833(1997).
 RN [10]
 RP PROCESSING.
 RX MEDLINE=98087475; PubMed=9427603;
 RA Tanaka M., Itai T., Adachi M., Nagata S.:
 RT "Downregulation of Fas ligand by shedding.";
 RL Nat. Med. 4:31-36(1998).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/Dec3
 CC modulates its effects.
 CC -1- SUBUNIT: Homotrimer (Probable).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. May be released
 CC into the extracellular fluid, probably by cleavage form the cell
 CC surface.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P48023-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P48023-2; Sequence=VSP_006443, VSP_006444;
 CC -1- PTM: N-glycosylated.
 CC -1- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing.
 CC -1- DISEASE: Defects in TNFRSF6 are a cause of autoimmune
 CC lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
 CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome

CC involving hemolytic anemia and thrombocytopenia with massive
 CC lymphadenopathy and splenomegaly.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -1- DATABASE: NAME=PROW, NOTE=PROW 2:59-69(2001);
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb.ch).
 CC -----
 CC EMBL: X89102; CAA61474.1; -;
 CC EMBL: U08137; AAC50071.1; -;
 CC EMBL: U11821; AAC50124.1; -;
 CC EMBL: D38122; BAA07320.1; -;
 CC EMBL: AF288573; AAG60017.1; -;
 CC EMBL: Z96050; CAB09424.1; -;
 CC EMBL: BC017502; AAB17502.1; -;
 CC EMBL: AB013303; BAA2542.1; -;
 CC F1R: I38707; I38707.
 CC HSP: P50591; I02Q.
 CC Genew: HGNC:11936; TNFRSF6.
 CC H-Invdb: HIX001337; -;
 CC MIM: 134638; -;
 CC MIM: 601859; -;
 CC GO: GO:0005887; C: integral to plasma membrane; TAS.
 CC GO: GO:0005102; P: receptor binding; TAS.
 CC GO: GO:0007267; P: cell-cell signaling; TAS.
 CC GO: GO:0006917; P: induction of apoptosis; TAS.
 CC GO: GO:0043123; P: positive regulation of I-kappa kinase/NF-kappaB; IEF.
 CC GO: GO:0007165; P: signal transduction; TAS.
 CC InterPro: IPR008064; Fas_ligand.
 CC InterPro: IPR006053; TNF_abc.
 CC InterPro: IPR006052; TNF_family.
 CC InterPro: IPR008983; TNF_1like.
 CC InterPro: IPR003636; TNF_subf.
 CC Pfam: PF00229; TNF_1.
 CC PRINTS: PR01681; FASLIGAND.
 CC PRINTS: PR01234; TNFCROSISFCT.
 CC ProDom: PD002012; TNF_subf. 1.
 CC PROSITE: PS00251; TNF_1; 1.
 CC PROSITE: PS50049; TNF_2; 1.
 CC KW Alternative splicing; Antigen; Apoptosis; Cytokine; Glycoprotein;
 CC Signal-anchor; Transmembrane.
 CC CHAIN 1 281
 CC FT
 CC CHAIN 130 281
 CC FT
 CC DOMAIN 1 80
 CC FT
 CC TRANSMEM 81 102
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 CC DOMAIN 103 281
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 CC CARBOHYD 260 260
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 CC VARSPLIC 117 127
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 CC FT
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 CC MUTAGEN 275 275
 CC FT

Missing (in isoform 2).
 /FTid=VSP_006443.
 /FTid=VSP_006444.
 P->D,F,R: Lowers binding to TNFRSF6 and
 reduces cytotoxicity more than 100-fold.
 Y->S,R: Lowers binding to TNFRSF6 and
 abolishes cytotoxicity.
 F->L: Abolishes binding to TNFRSF6 and
 cytotoxicity.

SQL SEQUENCE 281 AA; 31485 MW; A8A6EB358246E9BB CRC64;

Query Match 12.6%; Score 186; DB 1; Length 281;

Best Local Similarity 22.1%; Fred. No. 4.9e-07;

Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

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OY 4 MEVGGPSLIGTCVLIVIFTVLLQSLCVAV---TYVYFTNELKQMDKYSKSGIACFLKE 60
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 71 LKRGHNSTG-LCLVMEFVVALVGLGSLGMFOLHLOKELAELEBESTQKHTASLEK 129
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY 61 DDSYWDPNDEESMNSPCWQVKNQOLVKNMILRTSEETISTVQEKQONISPLVREGRPO 120
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 130 QIGHSPPPPE-----KKELRKV----- 146
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSRSGHSFLSNLHNGELVIHENG 180
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 147 ---AHLT---GRSNRSRMP-----LEWEDT-YGIVLLSGVKYKKGGLVINETG 187
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY 181 FYIYSQTYFRFOEIKENTKNDKQNVQIY-KYTSYDPDILLMKSRNS-----CWGK 233
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 188 LYFVTSKYVFRQ-----SCNNLPUSHKVKYVRNSKYFODLVMEGKMMSYCTTGOMMAR 241
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY 234 DAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAP 278
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 242 -----SSYLGAVFNLTSADHLVYVNSELSLVNFEESQTFFGLY 279
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Search completed: March 2, 2005, 14:50:42
Job time : 179 secs

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OM protein - protein search, using sw model

Run on: March 2, 2005, 14:50:47 ; Search time 25 Seconds
(without alignments)
505.326 Million cell updates/sec

Title: US-10-077-435-1
Perfect score: 1478
Sequence: 1 MAMMEVGGPSLGGTCTVLIV.....NEHLIDMDHESFPGAFVLG 281

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 181127 seqs, 44957854 residues
Total number of hits satisfying chosen parameters: 181127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New:
1: /cgn2_6/ptodata/2/paa/BCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US05_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
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6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
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8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	US-10-077-435-1	Sequence 1, Appl.
2	1478	100.0	281	US-11-028-780-20	Sequence 20, Appl.
3	813	55.0	163	US-10-839-694A-4	Sequence 4, Appl.
4	251.5	17.0	317	US-11-028-780-22	Sequence 22, Appl.
5	230.5	15.6	170	US-09-791-153E-157	Sequence 157, App
6	228.5	15.5	155	US-10-839-694A-6	Sequence 6, Appl.
7	186	12.6	281	US-11-028-780-112	Sequence 12, Appl.
8	186	12.6	281	US-11-054-539-6	Sequence 38, Appl.
9	166	11.2	251	US-11-028-780-38	Sequence 38, Appl.
10	160	10.8	174	US-11-028-780-36	Sequence 36, Appl.
11	159.5	10.8	240	US-11-028-780-34	Sequence 34, Appl.
12	149.5	10.1	260	US-10-916-286A-73	Sequence 73, Appl.
13	147.5	10.0	260	US-10-916-286A-65	Sequence 65, Appl.
14	147.5	10.0	261	PCT-US05-02350-136	Sequence 136, App
15	147.5	10.0	261	US-11-021-951-143	Sequence 143, Appl
16	147.5	10.0	261	US-11-028-780-10	Sequence 10, Appl
17	147.5	10.0	261	US-11-043-770-136	Sequence 136, App
18	147.5	10.0	263	US-10-450-763-52743	Sequence 52743, A
19	136.5	9.2	211	US-10-916-286A-78	Sequence 78, Appl
20	134.5	9.1	211	US-10-916-286A-70	Sequence 70, Appl
21	125.5	8.5	233	PCT-US05-02350-1147	Sequence 1147, App
22	125.5	8.5	233	PCT-US05-02350-1155	Sequence 1155, App
23	125.5	8.5	233	US-11-028-780-4	Sequence 4, Appl.
24	125.5	8.5	233	US-11-043-770-1147	Sequence 1147, App
25	125.5	8.5	233	US-11-043-770-1155	Sequence 1155, App

26	125.5	8.5	233	7	US-11-054-539-3	Sequence 3, Appl.
27	125.5	8.5	233	8	US-60-643-337-4	Sequence 4, Appl.
28	122	8.3	144	6	US-10-839-694A-3	Sequence 3, Appl.
29	122	8.3	205	7	US-11-033-545-304	Sequence 304, App
30	122	8.3	205	7	US-11-028-780-2	Sequence 2, Appl.
31	122	8.3	205	7	US-11-054-539-4	Sequence 4, Appl.
32	122	8.3	217	1	PCT-US05-02350-1146	Sequence 1146, App
33	122	8.3	217	7	US-11-043-770-1146	Sequence 1146, App
34	122	8.3	251	7	US-11-033-545-541	Sequence 541, App
35	119.5	8.1	240	1	PCT-US05-02350-137	Sequence 137, App
36	119.5	8.1	240	7	US-11-043-770-137	Sequence 137, App
37	118	8.0	240	1	PCT-US05-02350-326	Sequence 326, App
38	118	8.0	240	7	US-11-043-770-326	Sequence 326, App
39	117	7.9	146	6	US-10-839-694A-5	Sequence 5, Appl.
40	117	7.9	152	6	US-10-839-694A-2	Sequence 2, Appl.
41	116.5	7.9	157	5	US-09-920-137C-9	Sequence 9, Appl.
42	116.5	7.9	157	5	US-09-927-703A-1	Sequence 1, Appl.
43	116.5	7.9	157	6	US-10-697-628B-9	Sequence 9, Appl.
44	116.5	7.9	157	6	US-10-954-900A-9	Sequence 9, Appl.
45	116.5	7.9	157	7	US-11-053-750-1	Sequence 1, Appl.

ALIGNMENTS

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RESULT 1
US-10-077-435-1
; Sequence 1, Application US/10077435
; GENERAL INFORMATION:
; APPLICANT: Kumar, M. Vijay
; TITLE OF INVENTION: Treatment of Prostate Cancer
; FILE REFERENCE: M0351-268908
; CURRENT APPLICATION NUMBER: US/10/077,435
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,698
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-435-1

Query Match      100.0%; Score 1478; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 4.1e-129;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      121 RVAAHITTRGRSNTLSSPNSKNEKALCKKINSMESSSGSFLSNLRLNGELVIHKG 180
DB      121 RVAAHITTRGRSNTLSSPNSKNEKALCKKINSMESSSGSFLSNLRLNGELVIHKG 180
QY      181 FVYISQYFFPFOEIKENTKNDKQOVYIKYTSYPPPIILMSARNSCKDAEYGLY 240
DB      181 FVYISQYFFPFOEIKENTKNDKQOVYIKYTSYPPPIILMSARNSCKDAEYGLY 240
QY      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHESFPGAFVLG 281
DB      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHESFPGAFVLG 281

RESULT 2
US-11-028-780-20
; Sequence 20, Application US/11028780
; GENERAL INFORMATION:
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/ APPLICANT: Human Genome Sciences, Inc.,
/ TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
/ FILE REFERENCE: PF559C1
/ CURRENT APPLICATION NUMBER: US/11/028,780
/ PRIOR FILING DATE: 2005-01-05
/ PRIOR APPLICATION NUMBER: 10/202,062
/ PRIOR FILING DATE: 2002-07-25
/ PRIOR APPLICATION NUMBER: 60/307,838
/ PRIOR FILING DATE: 2001-07-27
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 20
/ LENGTH: 281
/ TYPE: PRT
/ ORGANISM: human
US-11-028-780-20

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Best Local Similarity 100.0%; Pred. No. 4,1e-129;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 DDSYVDPNDESMNSPCQVQKQLRQVYKMLRTSEETISTVQEKQONISPLVERGPO 120
DB 61 DDSYVDPNDESMNSPCQVQKQLRQVYKMLRTSEETISTVQEKQONISPLVERGPO 120
QY 121 RYAAHITGTGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLNHLRNGELVTHEG 180
DB 121 RYAAHITGTGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLNHLRNGELVTHEG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYPPDILMKSAARNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYPPDILMKSAARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPFLVG 281

RESULT 3
US-10-839-694A-4
/ Sequence 4, Application US/10839694A
/ GENERAL INFORMATION:
/ APPLICANT: Li, Yuling
/ APPLICANT: Oren, Deena
/ APPLICANT: Arnold, Edward
/ APPLICANT: Volovik, Yulia
/ TITLE OF INVENTION: Crystalline Neutrokin-alpha Protein, Method of preparation
/ FILE REFERENCE: PF567
/ CURRENT APPLICATION NUMBER: US/10/839,694A
/ CURRENT FILING DATE: 2004-05-06
/ PRIOR APPLICATION NUMBER: PCT/US02/35661
/ PRIOR FILING DATE: 2002-11-07
/ PRIOR APPLICATION NUMBER: 60/331,049
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 4
/ LENGTH: 163
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (15)..(15)
/ OTHER INFORMATION: Xaa equals Ser; omitted at asterisk in TRAIL sequence depicted in
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (16)..(16)

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/ OTHER INFORMATION: Xaa equals Asn; omitted at asterisk in TRAIL sequence depicted in
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/ LOCATION: (17)..(17)
/ OTHER INFORMATION: Xaa equals Thr; omitted at asterisk in TRAIL sequence depicted in
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/ OTHER INFORMATION: Xaa equals Leu; omitted at asterisk in TRAIL sequence depicted in
/ OTHER INFORMATION: Figure 1
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
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/ LOCATION: (21)..(21)
/ OTHER INFORMATION: Xaa equals Pro; omitted at asterisk in TRAIL sequence depicted in
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/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (22)..(22)
/ OTHER INFORMATION: Xaa equals Asn; omitted at asterisk in TRAIL sequence depicted in
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/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (23)..(23)
/ OTHER INFORMATION: Xaa equals Ser omitted at asterisk in TRAIL sequence depicted in
/ OTHER INFORMATION: Figure 1
US-10-839-694A-4

Query Match      55.0%; Score 813; DB 6; Length 163;
Best Local Similarity 94.5%; Pred. No. 6,2e-68;
Matches 154; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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DB 1 PQRYAAHITGTGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLNHLRNGELVTHE 178
QY 179 KGFYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYPPDILMKSAARNSCWSKDAEYGLY 238
DB 61 KGFYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYPPDILMKSAARNSCWSKDAEYGLY 238
QY 239 LYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPFLVG 281
DB 121 LYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPFLVG 163

RESULT 4
US-11-028-780-22
/ Sequence 22, Application US/11028780
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc.,
/ TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
/ FILE REFERENCE: PF559C1
/ CURRENT APPLICATION NUMBER: US/11/028,780
/ CURRENT FILING DATE: 2005-01-05
/ PRIOR APPLICATION NUMBER: 10/202,062
/ PRIOR FILING DATE: 2002-07-25
/ PRIOR APPLICATION NUMBER: 60/307,838
/ PRIOR FILING DATE: 2001-07-27
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 22
/ LENGTH: 317

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; TYPE: PRT
; ORGANISM: human
US-11-028-780-22

Query Match      17.0%; Score 251.5; DB 7; Length 317;
Best Local Similarity 24.1%; Pred. No. 1.2e-15;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

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DB 42 PAAASHMFAALGLGIGQVCSVALFFYRAQND--PNKISBDGTCYIRILRLHENDAF 99
OY 62 -DSYDNDPDEESMNSPCQVKN-----QLRQLVRKILRTSEETI-----STVOEKO 107
DB 100 QDTLIESQDTKILPDSCKRIKQAFQAGVQKELQHVSGHIAEKAMVSGMIDLAKRSK 159
OY 108 QNISPLVBERGQFQVAHAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSL 167
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OY 168 HLRNDELVIHEKGFYIYISQYFRPOEIKENTKNDKQVQIYKYT-SYDPDILMKSA 226
DB 200 TFSNCKLIVNQDGFYLLVYANICFRHHETSGDLATEYLQLMVYVTKSIKIPSSHTLMKG 259
OY 227 RNSCKDAEYGLYSIYQGIFFELKENDRIFVSVTNEHLIDMDHEASFGAFV 280
DB 260 STKWSGNSERHFYSINVGGFKLRSGERISIEVSNPSLDDPDATYFGAFV 313

RESULT 5
US-09-791-153E-157
; Sequence 157, Application US/09791153E
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra V.
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William J.
; APPLICANT: Sullivan, John K.
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153E
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 157
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153E-157

Query Match      15.6%; Score 230.5; DB 5; Length 170;
Best Local Similarity 34.2%; Pred. No. 4.6e-14;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

OY 124 AHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSLRLNDELVIHEKGFY 183
DB 19 AHLT-----INAAISPSGSHKVTL--SSWYHDR-GMAKISMTLNSGLRNVNQDGFY 68
OY 184 IYSQYFRPOEIKENTKNDKQVQIYKYT-SYDPDILMKSA RNSCKDAEYGLYSI 242
DB 69 LVANICFRHHETSGDLATEYLQLMVYVTKSIKIPSSHTLMKGSTKWSGNSERHFYSI 128
OY 243 YQGIFFELKENDRIFVSVTNEHLIDMDHEASFGAFV 280
DB 129 NVGGFFKLRSGERISIEVSNPSLDDPDATYFGAFV 316

RESULT 6
US-10-839-694A-6
; Sequence 6, Application US/10839694A
; GENERAL INFORMATION:
; APPLICANT: Li, Yuling

```

```

; APPLICANT: Oren, Deena
; APPLICANT: Arnold, Edward
; APPLICANT: Volovik, Yulia
; TITLE OF INVENTION: Crystalline Neurokinine-alpha Protein, Method of preparation
; FILE REFERENCE: PF567
; CURRENT APPLICATION NUMBER: US/10/839,694A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: PCT/US02/35661
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/331,049
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-839-694A-6

Query Match      15.5%; Score 228.5; DB 6; Length 155;
Best Local Similarity 34.2%; Pred. No. 6.3e-14;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

OY 124 AHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSLRLNDELVIHEKGFY 183
DB 4 AHLT-----INAAISPSGSHKVTL--SSWYHDR-GMAKISMTLNSGLRNVNQDGFY 53
OY 184 IYSQYFRPOEIKENTKNDKQVQIYKYT-SYDPDILMKSA RNSCKDAEYGLYSI 242
DB 54 LVANICFRHHETSGVPTDYQLQLMVYVTKSIKIPSSHTLMKGSTKWSGNSERHFYSI 113
OY 243 YQGIFFELKENDRIFVSVTNEHLIDMDHEASFGAFV 280
DB 114 NVGGFFKLRSGERISIEVSNPSLDDPDATYFGAFV 315

RESULT 7
US-11-028-780-12
; Sequence 12, Application US/11028780
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559C1
; CURRENT APPLICATION NUMBER: US/11/028,780
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 10/202,062
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-11-028-780-12

Query Match      12.6%; Score 186; DB 7; Length 281;
Best Local Similarity 22.1%; Pred. No. 1.1e-09;
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

OY 4 MEVQGPSLQTCVLIVFTVLQSLCAV---TVYFTNELKQMDKXSGIACFLKE 60
DB 71 LKKRGHSTG-LCLVMFMTVLVALVGLGIFOLFOKELAELESTQHTASSLEK 129
OY 61 DSYDNDPDEESMNSPCQVKNQLRQLVRKILRTSEETISTVOEQQVNSPLVBERGQ 120
DB 130 QIHPSRPP-----KELARKV----- 146
OY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSLRLNDELVIHEKGFY 180
DB 147 ---AHLT---GKNSRSM-----LEWEDT-YGIVLGSGVKKKGLVYINENG 187

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Qy 263 EHLIDMDHE-ASFGGAFV 280
 Db 156 ISLVDTKEDKTFGAFEL 174

RESULT 11

US-11-028-780-34
 ; Sequence 34, Application US/11028780
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc.,
 ; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
 ; FILE REFERENCE: PF559C1
 ; CURRENT APPLICATION NUMBER: US/11/028,780
 ; PRIOR FILING DATE: 2005-01-05
 ; PRIOR APPLICATION NUMBER: 10/202,062
 ; PRIOR FILING DATE: 2002-07-25
 ; PRIOR APPLICATION NUMBER: 60/307,838
 ; PRIOR FILING DATE: 2001-07-27
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 34
 ; LENGTH: 240
 ; TYPE: PRT
 ; ORGANISM: human
 US-11-028-780-34

Query Match 10.8%; Score 159.5; DB 7; Length 240;
 Best Local Similarity 23.8%; Pred. No. 2.6e-07;
 Matches 53; Conservative 41; Mismatches 66; Indels 63; Gaps 9;

Qy 79 QYKWLRLVLRKMLRTSEETITVQEKQON--ISPLVRERGPORVAHITGRGENTLS 137
 Db 60 QHMRKGEVNTLPPGPGASWEQLDERKSHVNP-----AAHLIGANSSLTGSG 109
 Qy 138 SPNSKNEKALGRKINSMESSRSQHSFLSNLHRLNGELVIHEKGFYIYSGTYFRFOEIK 197
 Db 110 GP-----LIME-TQLGLATLRGLSYHDGLVLTAKGYIYISK----- 146
 Qy 198 ENTQDKQNVQY-----IYKLT-STPDPILMKKARNSCMSDAEYGL 240
 Db 147 -----VOLGVGCPGLASTITHGLYKTRPRYPELELIVSQSPCGRATSSRYV 197
 Qy 241 --SIYGGIFELKENDRIFVSVTNEHLIDM--DHEASFGAFV 280
 Db 198 WDSFUGVYVHLAGEEVRVDERLVRLDGTSYFGAFV 240

RESULT 12

US-10-916-286A-73
 ; Sequence 73, Application US/10916286A
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Gek-Kee
 ; APPLICANT: Drelitz, Matthew J.
 ; TITLE OF INVENTION: CANINE IL-4 IMMUNOREGULATORY PROTEINS AND USES THEREOF
 ; FILE REFERENCE: IM-2-CI-R
 ; CURRENT APPLICATION NUMBER: US/10/916,286A
 ; PRIOR FILING DATE: 2004-08-11
 ; PRIOR APPLICATION NUMBER: 09/322,409
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/087,306
 ; PRIOR FILING DATE: 1998-05-29
 ; NUMBER OF SEQ ID NOS: 154
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 73
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Felis catus
 US-10-916-286A-73

Query Match 10.1%; Score 149.5; DB 6; Length 260;
 Best Local Similarity 24.4%; Pred. No. 2.4e-06;
 Matches 69; Conservative 57; Mismatches 114; Indels 43; Gaps 15;

Qy 2 AMMEVQGPSLQGTCLVLIPTVLL--QSLCAVATVYVFTNELKQMODKYSKGIACFLK 59
 Db 9 APRSVATGPVPVSMK-IFWVLTIVFLITQWIGSALPAVYIHRRLDKIEDERNLYEDVPVFK 67
 Qy 60 EDDSYWDPNDEESMNS--PCWQVQWQLRQVLRKMLRTSEETITVQEKQONISPLVRER 117
 Db 68 ---TLQCKNKGSGSLNLCSEIKSFQFAFLKEIML--NKET-----KKEKVA--MOK 114
 Qy 118 GPQ--RVAAHITGTRGSTLTSSPNSKNEKALGRKINSMESSRSQHSFLSNL-HLNG-E 173
 Db 115 GQDDPRVAHV-----ISEASSSTASVL-----QW-ARKGYTTSSNLVTLLENGQ 159
 Qy 174 LVTHKGFYIYSGTYFRFOEIKENTKNDKQWQIYKYTSYPPDILMKARNSCWSK 233
 Db 160 LAVKQGLYIYAQVTFPCNRE-----ASSQAFVSLCHSPSGSERVILRAANRSSSK 215
 Qy 234 DAEVGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFG 276
 Db 216 PC--GQOSIHLGVEFLHPGASVFNVTDPQSVSHGTGFTSPG 256

RESULT 13

US-10-916-286A-65
 ; Sequence 65, Application US/10916286A
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Gek-Kee
 ; APPLICANT: Drelitz, Matthew J.
 ; TITLE OF INVENTION: CANINE IL-4 IMMUNOREGULATORY PROTEINS AND USES THEREOF
 ; FILE REFERENCE: IM-2-CI-R
 ; CURRENT APPLICATION NUMBER: US/10/916,286A
 ; PRIOR FILING DATE: 2004-08-11
 ; PRIOR APPLICATION NUMBER: 09/322,409
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/087,306
 ; NUMBER OF SEQ ID NOS: 154
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 65
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Canis familiaris
 US-10-916-286A-65

Query Match 10.0%; Score 147.5; DB 6; Length 260;
 Best Local Similarity 24.0%; Pred. No. 3.7e-06;
 Matches 68; Conservative 55; Mismatches 117; Indels 43; Gaps 14;

Qy 2 AMMEVQGPSLQGTCLVLIPTVLL--QSLCAVATVYVFTNELKQMODKYSKGIACFLK 59
 Db 9 APRSVATGPVPVSMK-IFWVLTIVFLITQWIGSALPAVYIHRRLDKIEDERNLYEDVPVFK 67
 Qy 60 EDDSYWDPNDEESMNS--PCWQVQWQLRQVLRKMLRTSEETITVQEKQONISPLVRER 117
 Db 68 ---TLQCKNKGSGSLNLCSEIKSFQFAFLKEIMLNE-----MKKEENIA--MOK 114
 Qy 118 GPQ--RVAAHITGTRGSTLTSSPNSKNEKALGRKINSMESSRSQHSFLSNL-HLNG-E 173
 Db 115 GQDDPRVAHV-----SEASSNPAS-----VLRN-ARKGYTTSSNLVTLLENGQ 159
 Qy 174 LVTHKGFYIYSGTYFRFOEIKENTKNDKQWQIYKYTSYPPDILMKARNSCWSK 233
 Db 160 LAVKQGLYIYAQVTFPCNRA-----ASSQAFVSLCHSPSGSERVILRAANRSSSK 215
 Qy 234 DAEVGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFG 276
 Db 216 PC--GQOSIHLGVEFLHPGASVFNVTDPQSVSHGTGFTSPG 256

RESULT 14

PCT-US05-02350-136
 ; Sequence 136, Application PC/TUS0502350
 ; GENERAL INFORMATION:

```
/ APPLICANT: Ayalon-Soffer, Michael
/ APPLICANT: Levine, Zurit
/ APPLICANT: Sella-Tavor, Osnat
/ APPLICANT: Diber, Alex
/ APPLICANT: Shemesh, Ronen
/ APPLICANT: Toporik, Amir
/ APPLICANT: Rotman, Galit
/ APPLICANT: Nemzer, Sergey
/ APPLICANT: Rosenberg, Avi
/ APPLICANT: Dahary, Dvir
/ APPLICANT: Wool, Assaf
/ APPLICANT: Cojocaru, Gad S.
/ APPLICANT: Akiya, Pinchas
/ APPLICANT: Pollock, Sarah
/ APPLICANT: Savitsky, Klmaret
/ APPLICANT: Bernstein, Jeanne
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING
/ TITLE OF INVENTION: SAME
/ FILE REFERENCE: 28487
/ CURRENT APPLICATION NUMBER: PCT/US05/02350
/ CURRENT FILING DATE: 2005-02-10
/ NUMBER OF SEQ ID NOS: 1155
/ SOFTWARE: Patent version 3.3
/ SEQ ID NO 136
/ LENGTH: 261
/ TYPE: PRT
/ ORGANISM: Homo sapiens
PCT-US05-02350-136
```

```
Query Match 10.0%; Score 147.5; DB 1; Length 261;
Best Local Similarity 23.7%; Pred. No. 3.7e-06;
```

```
Matches 66; Conservative 51; Mismatches 99; Indels 63; Gaps 15;
```

```
QY 17 VLVIFTVLL--QSLCAVTVYFTNELKQMDKYSKGIACFLKEDDSYMPD-----ND 69
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 23 IFMYLTVFLITQMGSLFAVYLHRRLDKIEDERN-----LHEDFVFMKTICRNTG 75
70 EESNM-SPQWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRQVAHNTG 128
76 ERSLSLNCBEIKSKQEGFVQDIDL-NKET-----KENSFEMQKGDQNPQ-IAAHV-- 126
QY 129 TGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIEHKGYYIY 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 127 -----ISEASSKTTSVL-----QW--AEKGYTMSNNLVLENGKQLTVRKQGLYYIY 172
166 SQTFRFOBEIKENT-----KNDKQWQYIYKTTSTPDPILMKSRNCSKSDAEY 237
173 AQVTFCSNREASSQAPFLASLCLKSPGRFR-----ILLRANTHSSAKPC-- 218
QY 238 GLYSIYOGIFELKENDRIFVSVTNEHLIDMDHEASFPFG 276
DB 219 GQOSIHLGSGVFELQPGASVFVAVTDPDPSQVSHGTGFTSFG 257
```

```
RESULT 15
US-11-021-951-143
```

```
/ Sequence 143, Application US/11021951
```

```
/ GENERAL INFORMATION:
/ APPLICANT: HAUPTS, Ulrich
/ APPLICANT: KOLTERMANN, Andre
/ APPLICANT: SCHEIDIG, Andreas
/ APPLICANT: VOTSMEIER, Christian
/ APPLICANT: Ketting, Ulrich
/ APPLICANT: COCO, Wayne Michael
/ TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
/ FILE REFERENCE: 04156.0002U5
/ CURRENT APPLICATION NUMBER: US/11/021,951
/ CURRENT FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: 10/872,198
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 60/543,518
/ PRIOR FILING DATE: 2004-02-11
```

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/ PRIOR APPLICATION NUMBER: 60/524,960
/ PRIOR FILING DATE: 2003-11-25
/ PRIOR APPLICATION NUMBER: EP 04003058
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: EP 03025871
/ PRIOR FILING DATE: 2003-11-11
/ PRIOR APPLICATION NUMBER: EP 03025851
/ PRIOR FILING DATE: 2003-11-10
/ PRIOR APPLICATION NUMBER: EP 03013819
/ PRIOR FILING DATE: 2003-06-18
/ NUMBER OF SEQ ID NOS: 191
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 143
/ LENGTH: 261
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-021-951-143
```

```
Query Match 10.0%; Score 147.5; DB 7; Length 261;
```

```
Best Local Similarity 23.7%; Pred. No. 3.7e-06;
```

```
Matches 66; Conservative 51; Mismatches 99; Indels 63; Gaps 15;
```

```
QY 17 VLVIFTVLL--QSLCAVTVYFTNELKQMDKYSKGIACFLKEDDSYMPD-----ND 69
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 23 IFMYLTVFLITQMGSLFAVYLHRRLDKIEDERN-----LHEDFVFMKTICRNTG 75
70 EESNM-SPQWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRQVAHNTG 128
76 ERSLSLNCBEIKSKQEGFVQDIDL-NKET-----KENSFEMQKGDQNPQ-IAAHV-- 126
QY 129 TGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIEHKGYYIY 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 127 -----ISEASSKTTSVL-----QW--AEKGYTMSNNLVLENGKQLTVRKQGLYYIY 172
166 SQTFRFOBEIKENT-----KNDKQWQYIYKTTSTPDPILMKSRNCSKSDAEY 237
173 AQVTFCSNREASSQAPFLASLCLKSPGRFR-----ILLRANTHSSAKPC-- 218
QY 238 GLYSIYOGIFELKENDRIFVSVTNEHLIDMDHEASFPFG 276
DB 219 GQOSIHLGSGVFELQPGASVFVAVTDPDPSQVSHGTGFTSFG 257
```

```
Search completed: March 2, 2005, 15:03:38
Job time : 26 secs
```


PT Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
 PT apoptosis for the treatment of breast and colon cancer.

PS Claim 4; Fig 1a; 72pp; English.

CC A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian
 CC cell apoptosis. It is believed to be a member of the tumour necrosis
 CC factor cytokine family. Its amino acid sequence was deduced from a cDNA
 CC clone (AAT72796) isolated from a human placental cDNA library. Apo-2
 CC ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-
 CC 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells
 CC transformed or transfected with a vector contg. Apo-2 ligand nucleic
 CC acid. They can be used to induce apoptosis in mammals and to treat
 CC pathological conditions such as cancer (esp. breast or colon cancer) or
 CC to raise antibodies useful in diagnostic assays

SO Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
 Db 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DSDYNDPNDSESMNSPCQVQKQOLRQLVKRMILRTSEETISTVQEKQONISPLVERGQP 120
 Db 61 DSDYNDPNDSESMNSPCQVQKQOLRQLVKRMILRTSEETISTVQEKQONISPLVERGQP 120
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYYIYSQTYFRPQOEIKENTKNDKQVQIYKYTSYPPDILMKSAARNSCSKDAEYGLY 240
 Db 181 FYYIYSQTYFRPQOEIKENTKNDKQVQIYKYTSYPPDILMKSAARNSCSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 2
 AAW27134
 ID AAW27134 standard; protein; 281 AA.

AC AAW27134;

DT 02-APR-1998 (first entry)

DE Human Apoptosis inducing molecule-1 (AIM-1).

KW Apoptosis inducing molecule-1; AIM-1; autoimmune disorder;
 KW tumour necrosis factor ligand superfamily; AIM-1 altered expression;
 KW neoplasia inhibition; anti-inflammatory agent.

OS Homo sapiens.

PN WO9733899-A1.

PD 18-SEP-1997.

PF 14-MAR-1996; 96WO-US003773.

PR 14-MAR-1996; 96WO-US003773.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM;

WPI; 1997-470807/43.

DR N-PSDB; AAT85210.

XX New isolated apoptosis inducing molecule-1 - used to develop products for
 PT the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
 PT versus host disease or inflammation.

PS Claim 2; Fig 1; 82pp; English.

CC The present sequence represents a human Apoptosis inducing molecule-1
 CC (AIM-1). AIM-1 is a member of the tumour necrosis factor (TNF) ligand
 CC superfamily. The products can be used in the diagnosis and treatment of
 CC disorders related to under-expression, over-expression or altered
 CC expression of AIM-1. AIM-1 or agonists can be used for treating
 CC autoimmune disorders including systemic lupus erythematosus,
 CC immunoproliferative disease lymphadenopathy (ILD),
 CC angioimmunoproliferative lymphadenopathy (AIP), rheumatoid arthritis,
 CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit
 CC neoplasia such as tumour cell growth, to treat restenosis, to inhibit
 CC haematopoiesis in endothelial cell development, to stimulate peripheral
 CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
 CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or
 CC osteoporosis, for preventing graft-host rejection, and as anti-
 CC inflammatory agents, for treating endotoxin shock or to prevent
 CC activation of HIV

SO Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
 Db 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DSDYNDPNDSESMNSPCQVQKQOLRQLVKRMILRTSEETISTVQEKQONISPLVERGQP 120
 Db 61 DSDYNDPNDSESMNSPCQVQKQOLRQLVKRMILRTSEETISTVQEKQONISPLVERGQP 120
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYYIYSQTYFRPQOEIKENTKNDKQVQIYKYTSYPPDILMKSAARNSCSKDAEYGLY 240
 Db 181 FYYIYSQTYFRPQOEIKENTKNDKQVQIYKYTSYPPDILMKSAARNSCSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 3
 AAW19787
 ID AAW19787 standard; protein; 281 AA.

AC AAW19787;

DT 24-SEP-1997 (first entry)

DE Human apoptosis inducer cytokine TRAIL.

KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
 KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
 KW thrombotic microangiopathy; therapy.

OS Homo sapiens.

XX

XX

XX

XX

Key Location/Qualifiers

FT 1..18 /label= Cytoplasmic_domain

FT 19..38 /label= Transmembrane_domain

FT 39..281


```

RESULT 5
AAM56760
ID AAM56760 standard; protein; 281 AA.
XX
XX AAM56760;
AC
XX
XX 05-AUG-1998 (first entry)
DT
XX
XX Human TRAIL polypeptide.
DE
XX
XX Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
XX cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX PH 1..18
XX FT /note= "N-terminal cytoplasmic domain"
XX FT Region 19..38
XX FT /note= "transmembrane region"
XX FT Domain 39..281
XX FT /note= "extracellular domain"
XX
XX US5763223-A.
XX
XX 09-JUN-1998.
XX
XX 25-JUN-1996; 96US-00670354.
XX
XX 29-JUN-1995; 95US-00496632.
XX PR 01-NOV-1995; 95US-00548368.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Goodwin RG, Wiley SR;
XX
XX WPI; 1998-347322/30.
XX DR N-PSDB; AAV29518.
XX
XX DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful
XX PT for producing recombinant polypeptides for research and therapy of
XX PT leukaemia, lymphoma, melanoma and viral infections.
XX
XX Claim 1; Col 33-36; 28pp; English.
XX
XX This represents a human tumour necrosis factor related apoptosis ligand
XX CC (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce
XX CC apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful
XX CC for producing the recombinant TRAIL polypeptides, which may be useful in
XX CC studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells
XX CC (e.g. to isolate antigens for vaccine development). The polypeptides can
XX CC be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal
XX CC treatment of blood or bone-marrow), or to treat viral infections
XX CC
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGSPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGSPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYNDPNDDESMNSPCWQVQKQOLVYKMTLRTSEETISTVQEQONISPLVBERGQ 120
Db 61 DDSYNDPNDDESMNSPCWQVQKQOLVYKMTLRTSEETISTVQEQONISPLVBERGQ 120
QY 121 RVAAHITGRRGSRNTLSSPNSKNEKALGKINSWESSRSGHSFLSYHLRNELVYHEHG 180
Db 121 RVAAHITGRRGSRNTLSSPNSKNEKALGKINSWESSRSGHSFLSYHLRNELVYHEHG 180

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QY 181 FYYIYSQTYFRFOEBIKENTKNDKQWQYIYKYTSYPPDPIILMKASRNSCWSKAEYGLY 240
Db 181 FYYIYSQTYFRFOEBIKENTKNDKQWQYIYKYTSYPPDPIILMKASRNSCWSKAEYGLY 240
QY 241 SIYOGIFELKENDRIFVSYTNEHLIDMDHEASFCAFLVG 281
Db 241 SIYOGIFELKENDRIFVSYTNEHLIDMDHEASFCAFLVG 281

RESULT 6
AAM44354
ID AAM44354 standard; protein; 281 AA.
XX
XX AAM44354;
AC
XX
XX 28-MAY-1998 (first entry)
DT
XX
XX Human AGP-1.
XX
XX Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;
XX bone resorption; haematopoietic disease.
XX
XX Homo sapiens.
XX
XX WO9746686-A2.
XX PN
XX 11-DEC-1997.
XX PD
XX
XX 06-JUN-1997; 97WO-US009895.
XX
XX 07-JUN-1996; 96US-00660562.
XX PR
XX (AMGE-) AMGEN INC.
XX
XX Johnson MJ, Simonet WS, Danilenko DM;
XX
XX WPI; 1998-042194/04.
XX DR N-PSDB; AAV15295.
XX
XX Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -
XX PT useful for treating inflammation, bone resorption and haematopoietic
XX PT diseases.
XX
XX Claim 7; Page 36-37; 54pp; English.
XX
XX The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis
XX CC factor (TNF)-related protein, involved in inflammation, myelopoiesis and
XX CC bone resorption. It has the same nucleic acid and amino acid (aa)
XX CC sequences as the TNF-related apoptosis-induced ligand (TRAIL) described
XX CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
XX CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
XX CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
XX CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
XX CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or
XX CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,
XX CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat
XX CC haematopoietic diseases associated with reduction in the number of bone
XX CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
XX CC by disease, injury or exposure to myelosuppressive agents. Host cells,
XX CC transformed with expression vectors containing AGP-1 DNA, are used to
XX CC produce recombinant AGP-1.
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGSPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGSPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60

```

QY 61 DSDYNDPNDDESMNSPCQVKKQLRQVYKMLRTSEETISTVQEKQONISPLVERBQ 120
 DB 61 DSDYNDPNDDESMNSPCQVKKQLRQVYKMLRTSEETISTVQEKQONISPLVERBQ 120
 QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRPQBEIKENTKNDKQVQYIYKTSYPPDILMKSGARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRPQBEIKENTKNDKQVQYIYKTSYPPDILMKSGARNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 7
 ID AAY01517 standard; peptide; 281 AA.
 AC AAY01517;
 DT 27-MAY-1999 (first entry)
 DE Protein associated with neurodegenerative and autoimmune diseases.
 XX Neurodegenerative disease; autoimmune disease; inflammatory disease;
 KM lupus erythematosus; rheumatoid arthritis; SFP; apoptotic;
 XX surface receptor; TRAIL protein.
 OS Homo sapiens.
 XX FR2766713-A1.
 PN 05-FEB-1999.
 PD 04-AUG-1997; 97FR-00010176.
 PF 04-AUG-1997; 97FR-00010176.
 PR 04-AUG-1997; 97FR-00010176.
 XX (INMR) BIO MERIEUX.
 PA Rieger F, Belliveau JF, Perron H;
 PI WPI; 1999-156177/14.
 DR Use of polypeptide derived from TRAIL protein for diagnosis of
 PT degenerative disease - autoimmunity and inflammation, also useful in
 PT prevention or treatment, and similar use of corresponding ligand and
 PT nucleic acid.
 PS Claim 2; Page 13; 21pp; French.
 XX The specification describes the use of a polypeptide corresponding to at
 CC least the primary sequence of part of the present sequence to produce a
 CC diagnostic, prophylactic or therapeutic composition useful in cases of
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
 CC be used in treatment of neurodegenerative diseases, lupus erythematosus,
 CC rheumatoid arthritis, and SFP. The polypeptides are apoptotic in central
 CC nervous system cells, antigenic and specifically recognise the surface
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
 CC receptors, inhibiting formation of natural complex
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAMEVQGGPSLQGTCLVIVFTVLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60

DB 1 NAMEVQGGPSLQGTCLVIVFTVLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DSDYNDPNDDESMNSPCQVKKQLRQVYKMLRTSEETISTVQEKQONISPLVERBQ 120
 DB 61 DSDYNDPNDDESMNSPCQVKKQLRQVYKMLRTSEETISTVQEKQONISPLVERBQ 120
 QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRPQBEIKENTKNDKQVQYIYKTSYPPDILMKSGARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRPQBEIKENTKNDKQVQYIYKTSYPPDILMKSGARNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 8
 ID AAY27012 standard; protein; 281 AA.
 AC AAY27012;
 DT 24-SEP-1999 (first entry)
 DE Human Apo-2 ligand (Apo-2L) polypeptide.
 XX Cytochrome; Apo-2L; apoptosis; cancer; autoimmune disorder;
 KM lupus; immune-mediated glomerular nephritis; human.
 XX Homo sapiens.
 OS WO9936535-A1.
 PN 22-JUL-1999.
 PD 15-JAN-1999; 99WO-US001039.
 PF 15-JAN-1999; 98US-00007886.
 PR 15-APR-1998; 98US-00060533.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Kelley RF, O'Connell MT, Plitt RM, Schwall RH;
 PI WPI; 1999-44397/37.
 DR N-PSDB; AAX86987.
 DR A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 PT in mammalian cancer cells.
 PS Claim 1; Fig 1A; 86pp; English.
 XX This sequence represents a novel human cytokine, designated Apo-2 ligand
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
QY 1 NAMEVQGSPSLGQTCVLIVITFTVLLQSLCAVAVTYVYFTNEKQKQDKYKSGIACFLKE 60
DB 1 NAMEVQGSPSLGQTCVLIVITFTVLLQSLCAVAVTYVYFTNEKQKQDKYKSGIACFLKE 60
QY 61 DSYNDPNDDESMNSPCQVQKQQLRVLRKMLRTSEETISTVOEKQNI SPLVBERGQ 120
DB 61 DSYNDPNDDESMNSPCQVQKQQLRVLRKMLRTSEETISTVOEKQNI SPLVBERGQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEBIKENTKDKQKVQYIYKTYSPDPILMKASRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEBIKENTKDKQKVQYIYKTYSPDPILMKASRNSCWSKDAEYGLY 240
QY 241 STYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 STYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
```

RESULT 9

AA81956
ID AA81956 standard; protein; 281 AA.

AA81956;

10-JUL-2000 (first entry)

Human Apo-2 ligand protein sequence.

Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
therapy; apoptosis; cancer.

Homo sapiens.

US6046048-A.

04-APR-2000.

08-JAN-1997; 97US-00780496.

09-JAN-1996; 96US-0009755P.

(GETH) GENENTECH INC.

Kim KJ, Ashkenazi AJ, Chuntharapai A;

WPI; 2000-282690/24.

N-PSDB; AAA07425.

New isolated monoclonal antibodies having antigen specificity for Apo-2
ligand, e.g. 2G6, 2B11 or 5G2, useful for detecting the expression of Apo
-2 ligand serum, and for treating diseases associated with increased
apoptosis.

Claim 9; Fig 1a; 46bp; English.

This sequence is the human Apo-2 ligand protein, which is recognised by
monoclonal antibodies produced by the hybridoma cell lines of the
invention. The hybridoma cell lines are deposited under the American Type
Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
tissues, or serum. The antibodies may also be employed as therapeutics.
For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
pathological conditions or diseases associated with increased apoptosis.
They are also useful for the affinity purification of Apo-2 ligand from
recombinant cell culture or natural sources. The Apo-2 ligand itself may
be used to treat diseases e.g. cancer, by inducing apoptosis in cells

Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 NAMEVQGSPSLGQTCVLIVITFTVLLQSLCAVAVTYVYFTNEKQKQDKYKSGIACFLKE 60
DB 1 NAMEVQGSPSLGQTCVLIVITFTVLLQSLCAVAVTYVYFTNEKQKQDKYKSGIACFLKE 60
QY 61 DSYNDPNDDESMNSPCQVQKQQLRVLRKMLRTSEETISTVOEKQNI SPLVBERGQ 120
DB 61 DSYNDPNDDESMNSPCQVQKQQLRVLRKMLRTSEETISTVOEKQNI SPLVBERGQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEBIKENTKDKQKVQYIYKTYSPDPILMKASRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEBIKENTKDKQKVQYIYKTYSPDPILMKASRNSCWSKDAEYGLY 240
QY 241 STYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 STYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
```

RESULT 10

AA824038
ID AA824038 standard; protein; 281 AA.

AA824038;

25-JAN-2001 (first entry)

Human PRO1096 protein sequence SEQ ID NO:51.

Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
identification; tumorigenesis; anticancer; detection.

Homo sapiens.

WO200053750-A1.

14-SEP-2000.

02-DEC-1999; 99WO-US028551.

08-MAR-1999; 99WO-US005028.

01-SEP-1999; 99WO-US020111.

29-OCT-1999; 99US-0162506P.

30-NOV-1999; 99WO-US028313.

01-DEC-1999; 99WO-US028634.

(GETH) GENENTECH INC.

Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WT;

WPI; 2000-594320/56.

N-PSDB; AAC58120.

Antibodies specific for PRO polypeptides, used to diagnose and inhibit
the growth of tumors in mammals, and to identify inhibitors of PRO
polypeptide activity or expression.

Claim 61; Fig 36; 226bp; English.

The present invention describes an antibody that binds to a human protein
(I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
PRO1927; PRO1567; PRO1293; PRO1303; PRO3444; PRO4354; PRO4397;
PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
activity and can be used to diagnose tumours in mammals, by detecting
complex formation when the antibody is contacted with test cells.
Increased expression of genes encoding (I) can also be detected to

CC diagnose tumours. Agents which inhibit the activity of (I), especially
 CC the antibodies, or an antisense oligonucleotide which hybridises to genes
 CC encoding (I), can be used to inhibit tumour growth, preferably by
 CC inducing cell death. Methods from the present invention can be used to
 CC identify compounds which inhibit the biological activity of (I). AAC58019
 CC to AAC58102 represent PCR primers and hybridisation probes used in
 CC examples from the present invention for human PRO sequences. AAC58103 to
 CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and
 CC protein sequences given in the exemplification of the present invention
 XX
 XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYNDPNDDESMNSPCQVQKQQLVRLVKMLRTSEETISTVOEKQONISPLVERGPQ 120
 DB 61 DDSYNDPNDDESMNSPCQVQKQQLVRLVKMLRTSEETISTVOEKQONISPLVERGPQ 120
 QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIHEKG 180
 DB 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSAARNSCMSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSAARNSCMSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 11

AAB08545
 ID AAB08545 standard; protein; 281 AA.

XX AAB08545;

DT 20-DEC-2000 (first entry)

XX Amino acid sequence of a human TRAIL polypeptide.

DE Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;

KW TNF related apoptosis-inducing ligand; tumour cell;

KM TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;

KW non-small cell lung carcinoma.

XX Homo sapiens.

OS WO200048619-A1.

XX 24-AUG-2000.

PF 15-FEB-2000; 2000WO-US003891.

XX 16-FEB-1999; 99US-0120313P.

PR (STRD) UNIV LELAND STANFORD JUNIOR.

XX Rosen GD;

PI MPI: 2000-558253/51.

XX N-PSDB; AAA64325.

XX Killing of tumor cells, e.g. solid tumors or carcinoma, comprises
 PT administration of synergistic combination of diterpenoid diepoxide and
 PT tumor necrosis factor related apoptosis-inducing ligand.
 XX

PS Disclosure; Page 23-24; 29pp; English.

XX The present sequence represents a human TRAIL (tumour necrosis factor
 CC (TNF) related apoptosis-inducing ligand) polypeptide. The specification
 CC describes a method for enhanced killing of tumour cells. The method
 CC comprises contacting a susceptible tumour cell with a synergistic mixture
 CC of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined
 CC dosage to kill at least 50 % of the cells. This mixture is synergistic,
 CC and so is active at lower doses and against otherwise resistant cell
 CC lines. The method is used for killing tumour cells, especially solid
 CC tumours or carcinomas (especially mammary carcinoma or non-small cell
 CC lung carcinoma)
 XX

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYNDPNDDESMNSPCQVQKQQLVRLVKMLRTSEETISTVOEKQONISPLVERGPQ 120
 DB 61 DDSYNDPNDDESMNSPCQVQKQQLVRLVKMLRTSEETISTVOEKQONISPLVERGPQ 120
 QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIHEKG 180
 DB 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSAARNSCMSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSAARNSCMSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 12

AAB28691
 ID AAB28691 standard; protein; 281 AA.

XX AAB28691;

DT 14-FEB-2001 (first entry)

XX Human AGP-1.

DE Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;

KW antiinflammatory; hepatocytic; antiarteriosclerotic; anti-HIV; HIV;

KM human immunodeficiency virus; apoptosis; proliferative disorder; cancer;

KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;

KM transplant rejection; cardiovascular disease; arteriosclerosis.

XX Homo sapiens.

OS WO200063253-A1.

XX 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US008004.

XX 16-APR-1999; 99US-00293245.

PR (AMGE-) AMGEN INC.

XX Hsu H, Meng S;

PI MPI: 2000-665240/64.

XX N-PSDB; AAC67831.

PT Fusion protein of Agp-1 protein and an Fc region, used to treat
PT proliferative disorders, immune disorders, and virally-induced disorders.
XX
XX Claim 3; Fig 2; 93pp; English.
XX
CC The present sequence is human Agp-1, a type II transmembrane protein.
CC Fusion proteins comprising an Fc immunoglobulin region fused to the N-
CC terminal portion of the Agp-1 protein have been produced. The fusion
CC proteins can be used to induce apoptosis in a tissue, and to treat
CC proliferative disorders, immune disorders, or virally-induced disorders.
CC The proliferative disorders include cancers, such as breast, prostate,
CC lung or colon cancer. The viral infections include hepatitis, and
CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
CC be autoimmune disorders or transplant rejection. Cardiovascular diseases
CC such as arteriosclerosis may also be treated. The Agp-1 containing fusion
CC proteins have increased biological activity compared to the soluble Agp-1
CC proteins used in prior art therapies
XX
SQ Sequence 281 AA:

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGSPSLGQTCVLIIVFTVLLQSLCAVATYYVFTNELKQMDKYSKGIACPLKE 60
DB 1 MAMMEVQGSPSLGQTCVLIIVFTVLLQSLCAVATYYVFTNELKQMDKYSKGIACPLKE 60
QY 61 DSYWDPNDEESMNSPCQVQKQOLVLRKMLRTSEETISTVQKQONISPLVERGQ 120
DB 61 DSYWDPNDEESMNSPCQVQKQOLVLRKMLRTSEETISTVQKQONISPLVERGQ 120
QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKTSYPPDILMKSRNSCWDKAEYGLY 240
DB 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKTSYPPDILMKSRNSCWDKAEYGLY 240
QY 241 SIYQGIIFELKENDRIFFSVTNEHLIDMDHEASFFGAPLVG 281
DB 241 SIYQGIIFELKENDRIFFSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 13
AAB50977
ID AAB50977 standard; protein; 281 AA.
XX
AC AAB50977;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO1096 protein.
XX
KW Human; PRO; cytosolic; neutrotropic; neuroprotective; respiratory general;
KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
XX
OS Homo sapiens.
XX
PN WO200073348-A2.
XX
PD 07-DEC-2000.
XX
PF 30-MAY-2000; 2000WO-US014941.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.

PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030055.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
XX
XX (GETH) GENENTECH INC.
XX
PA Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI,
XX
DR WPI, 2001-016509/02.
DR N-PSDB; AAC91579.
XX
PT Twenty eight nucleic acids encoding PRO polypeptides which are useful for
PT treating various tumors, e.g. breast cancer, and other inflammatory,
PT angiogenic and immunological disorders.
XX
PS Claim 31; Fig 54; 188pp; English.
XX
CC The present sequence is one of twenty eight novel PRO polypeptides. The
CC PRO polypeptides and their agonists, including antibodies, peptides, and
CC small molecule agonists, may be used to treat various tumors, e.g.,
CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
CC central nervous system cancer, melanoma or leukaemia. They are also
CC useful for treating other disorders such as neuronal, glial, astrocytal,
CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
CC blastocelic disorders, and inflammatory, angiogenic and immunological
CC disorders
XX
SQ Sequence 281 AA:

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGSPSLGQTCVLIIVFTVLLQSLCAVATYYVFTNELKQMDKYSKGIACPLKE 60
DB 1 MAMMEVQGSPSLGQTCVLIIVFTVLLQSLCAVATYYVFTNELKQMDKYSKGIACPLKE 60
QY 61 DSYWDPNDEESMNSPCQVQKQOLVLRKMLRTSEETISTVQKQONISPLVERGQ 120
DB 61 DSYWDPNDEESMNSPCQVQKQOLVLRKMLRTSEETISTVQKQONISPLVERGQ 120
QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKTSYPPDILMKSRNSCWDKAEYGLY 240
DB 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKTSYPPDILMKSRNSCWDKAEYGLY 240
QY 241 SIYQGIIFELKENDRIFFSVTNEHLIDMDHEASFFGAPLVG 281
DB 241 SIYQGIIFELKENDRIFFSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 14
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ID AAB67243 standard; protein; 281 AA.

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XX AC AAB67243;
XX 18-APR-2001 (first entry)
XX DE Human Apo2 ligand.
XX KW Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
XX OS Homo sapiens.
XX PN WO200100832-A1.
XX PD 04-JAN-2001.
XX PF 26-JUN-2000; 2000WO-US017579.
XX PR 28-JUN-1999; 99US-0141342P.
XX PA (GENTH ) GENENTECH INC.
XX PI Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
XX O'Connell M, Pai R, Shahrokh Z, Simmons L;
XX WPI; 2001-123012/13.
XX DR Use of divalent metal ions for making Apo-2 ligand and in formulations
XX PT containing Apo-2 ligand for increasing yield and stability of ligand
XX PT trimers, useful for therapeutic applications.
XX PS Claim 6; Fig 1; 60pp; English.
XX CC The present invention relates to a formulation comprising Apo-2 ligand
XX CC and divalent metal ions. Apo-2 ligand and the formulation are useful for
XX CC treating cancers and viral infections. Addition of divalent metal ions
XX CC for making Apo-2 ligand and formulations containing Apo-2 ligand results
XX CC in increased yield and stability of Apo-2 ligand trimers
XX SQ Sequence 281 AA;

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 DSYNDPNDDEESNNSPCQVQKQLRQLVKMLRTSEETISTVQEKQONISPLVERGPO 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNRNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNRNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKDKQVQIYIKTSTPDPILMKSRNSCWSKDAEYGLY 240
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QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFAPFLVG 281
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RESULT 15
AAE11031
ID AAE11031 standard; protein; 281 AA.
XX AAE11031;
AC AAE11031;
XX 18-DEC-2001 (first entry)
XX

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DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
XX Human; tumour necrosis factor; TNF; cytokine; cytotoxic; virucide;
XX TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
XX human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
XX melanoma.
XX OS Homo sapiens.
XX PN US6284236-B1.
XX PD 04-SEP-2001.
XX PF 26-MAY-1999; 99US-00320424.
XX PR 29-JUN-1995; 95US-00496632.
XX PR 01-NOV-1995; 95US-00548368.
XX PR 25-JUN-1996; 96US-00670354.
XX PR 26-MAR-1998; 98US-00048641.
XX PR 10-NOV-1998; 98US-00190046.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Wiley SR, Goodwin RG;
XX WPI; 2001-595463/67.
XX DR N-PSDB; AAD18395.
XX PT New tumor necrosis factor related apoptosis inducing ligand polypeptides
XX PT for treating viral infections (e.g. bovine viral diarrhoea or human
XX PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
XX PS Claim 2; Col 45-48; 41pp; English.
XX CC The invention relates to a cytokine designated as tumour necrosis factor
XX CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
XX CC of certain target cells, including cancer cells and virally infected
XX CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
XX CC treating viral infections (e.g. bovine viral diarrhoea or human
XX CC immunodeficiency virus (HIV) and cancers (e.g. leukaemia, lymphoma and
XX CC melanoma), as a research reagent useful in studying apoptosis including
XX CC the regulation of programmed cell death. TRAIL DNA sequences may be
XX CC employed in developing a gene therapy approach to treating disorders
XX CC mediated by defective or insufficient amounts of TRAIL, in the production
XX CC of TRAIL polypeptides and as probes or primers in polymerase chain
XX CC reactions (PCR). The present sequence is human TRAIL protein
XX SQ Sequence 281 AA;

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGGTCVLIVITVLLQSLCAVNTVYVFNELKQMDKSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGGTCVLIVITVLLQSLCAVNTVYVFNELKQMDKSKSGIACFLKE 60
QY 61 DSYNDPNDDEESNNSPCQVQKQLRQLVKMLRTSEETISTVQEKQONISPLVERGPO 120
DB 61 DSYNDPNDDEESNNSPCQVQKQLRQLVKMLRTSEETISTVQEKQONISPLVERGPO 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNRNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNRNGELVIHEKG 180

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 14:41:36 ; Search time 43 Seconds
(without alignments)
487.823 Million cell updates/sec

Title: US-10-077-435-1

Perfect score: 1478

Sequence: 1 MAMMEVQGGPSLGGTCVLIV.....NEHLIDMDHASFCAFLVG 281

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents, AA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1478	100.0	281	1	US-08-670-354-2
2	1478	100.0	281	3	US-08-584-031-1
3	1478	100.0	281	3	US-08-780-496-1
4	1478	100.0	281	3	US-08-883-086-10
5	1478	100.0	281	3	US-09-320-424-2
6	1478	100.0	281	3	US-09-333-593A-6
7	1478	100.0	281	4	US-09-157-864-11
8	1478	100.0	281	4	US-09-825-563-2
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14	1469	99.4	279	3	US-09-072-993C-3
15	1238	83.8	271	4	US-09-569-611C-30
16	988	66.8	253	3	US-09-320-424-11
17	988	66.8	253	4	US-09-825-563-11
18	988	66.8	256	3	US-09-320-424-13
19	988	66.8	256	4	US-09-825-563-13
20	930	62.9	177	3	US-09-105-343A-7
21	930	62.9	291	1	US-08-670-354-6
22	930	62.9	291	3	US-09-320-424-6
23	930	62.9	291	4	US-09-825-563-6
24	930	62.9	291	5	PCT-US96-10895-6
25	850	57.5	161	4	US-09-565-423-7
26	735	49.7	169	4	US-09-569-611C-29
27	654	44.2	183	3	US-09-105-343A-8

28	611	41.3	121	4	US-09-513-999C-7833	Sequence 7833, Ap
29	483	32.7	120	4	US-09-569-611C-32	Sequence 32, Appl
30	482	32.6	101	1	US-08-670-354-4	Sequence 4, Appl
31	482	32.6	101	3	US-09-320-424-4	Sequence 4, Appl
32	482	32.6	101	4	US-09-825-563-4	Sequence 4, Appl
33	482	32.6	101	5	PCT-US96-10895-4	Sequence 4, Appl
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36	258.5	17.5	294	3	US-08-995-659-11	Sequence 11, Appl
37	258.5	17.5	294	3	US-09-215-649A-11	Sequence 11, Appl
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41	258.5	17.5	294	4	US-09-466-496-11	Sequence 11, Appl
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44	258.5	17.5	294	4	US-09-877-650-11	Sequence 11, Appl
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ALIGNMENTS

RESULT 1
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-670-354-2
Query Match 100.0%; Score 1478; DB 1; Length 281;

[illegible]

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RESULT 2
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-584-031-1

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Qy	181	FYIYISQTYEFRFOEIKENTKNDKQOMQYIYKTYSPBPILMKSRARNSCWSKDAEYGLY	240		
Db	181	FYIYISQTYEFRFOEIKENTKNDKQOMQYIYKTYSPBPILMKSRARNSCWSKDAEYGLY	240		
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US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Arnan Chuntcharapai, Kyung Jin Kim

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	Query Match	100.0%	Score 1478	DB 3	length 281	
	Best Local Similarity	100.0%	Prod. No. 3.5e-149			
	Matches 281	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	1	MAMMEVGGPSLGCTCVLIVIFVTLVLOSICVAATVYVFTNELKQNDKRYSSGSIACFLKE	60			
Db	1	MAMMEVGGPSLGCTCVLIVIFVTLVLOSICVAATVYVFTNELKQNDKRYSSGSIACFLKE	60			
QY	61	DDSVWDNDDESNSSPCMQVEMQLRQVKKMILRTSEETISTVQEKQONIPLVAREGPQ	120			
Db	61	DDSVWDNDDESNSSPCMQVEMQLRQVKKMILRTSEETISTVQEKQONISPLVAREGPQ	120			
QY	121	RVAAHITGTRGRSTLTSSPNSKNEKALGRKINSWESSFSGHSFSLNHLRNGELVIYHEKG	180			
Db	121	RVAAHITGTRGRSTLTSSPNSKNEKALGRKINSWESSFSGHSFSLNHLRNGELVIYHEKG	180			
QY	181	FYYIYTSQTFPFQBEIKENTQNDKQVQYIKYTSYPPILIMKSARNSCSKDAEYGLY	240			
Db	181	FYYIYTSQTFPFQBEIKENTQNDKQVQYIKYTSYPPILIMKSARNSCSKDAEYGLY	240			
QY	241	SIYGGIIFELKENDRIFVSVTNEHLIMDHASFFGAFLVG	281			
Db	241	SIYGGIIFELKENDRIFVSVTNEHLIMDHASFFGAFLVG	281			

RESULT 4
 US-08-883-086-10
 ; Sequence 10, Application US/08883086
 ; Patent No. 6171787
 ; GENERAL INFORMATION:
 ; APPLICANT: WILEY, STEVEN
 ; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
 ; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ;

ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Porembek, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6171787e
US-08-883-086-10

Query Match 100.0%; Score 1478; DB 3; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.5e-149; Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVTVVFTNELKQMDKXSKGACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVTVVFTNELKQMDKXSKGACFLKE 60
QY 61 DDSYNDPNDDESMNSPCQVQKQQLVRLVKMLRTSEETISTVQKQONISPLVERGPQ 120
DB 61 DDSYNDPNDDESMNSPCQVQKQQLVRLVKMLRTSEETISTVQKQONISPLVERGPQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKDKQMVQYIYKTSYPPDILMKASRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKDKQMVQYIYKTSYPPDILMKASRNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 5
US-09-320-424-2

; Sequence 2, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; PRIOR FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368

; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 2:
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-09-320-424-2

Query Match 100.0%; Score 1478; DB 3; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.5e-149; Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVTVVFTNELKQMDKXSKGACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVTVVFTNELKQMDKXSKGACFLKE 60
QY 61 DDSYNDPNDDESMNSPCQVQKQQLVRLVKMLRTSEETISTVQKQONISPLVERGPQ 120
DB 61 DDSYNDPNDDESMNSPCQVQKQQLVRLVKMLRTSEETISTVQKQONISPLVERGPQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKDKQMVQYIYKTSYPPDILMKASRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKDKQMVQYIYKTSYPPDILMKASRNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 6
US-09-333-593A-6

; Sequence 6, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNER, ALEMESEGD
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; FILE REFERENCE: TR6
; CURRENT APPLICATION NUMBER: US/09/333,593A
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 281
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-333-593A-6

Query Match 100.0%; Score 1478; DB 3; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.5e-149; Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVTVVFTNELKQMDKXSKGACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVTVVFTNELKQMDKXSKGACFLKE 60

QY 61 DSDYDNDPNDSEMSPCQVQKQOLRQVLRKMLRTSEETISTVQEKQONISPLVERGPQ 120
DB 61 DSDYDNDPNDSEMSPCQVQKQOLRQVLRKMLRTSEETISTVQEKQONISPLVERGPQ 120
QY 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHKG 180
DB 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQOVYIYKTSYPPDILMKSARNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQOVYIYKTSYPPDILMKSARNSCWSKDAEYGLY 240
QY 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHSAFFGAFVLG 281
DB 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHSAFFGAFVLG 281

RESULT 7
US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 611.1.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-09-157-864-11

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAMEVOGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
DB 1 NAMEVOGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
QY 61 DSDYDNDPNDSEMSPCQVQKQOLRQVLRKMLRTSEETISTVQEKQONISPLVERGPQ 120
DB 61 DSDYDNDPNDSEMSPCQVQKQOLRQVLRKMLRTSEETISTVQEKQONISPLVERGPQ 120

QY 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHKG 180
DB 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQOVYIYKTSYPPDILMKSARNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQOVYIYKTSYPPDILMKSARNSCWSKDAEYGLY 240
QY 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHSAFFGAFVLG 281
DB 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHSAFFGAFVLG 281

RESULT 8
US-09-825-563-2
; Sequence 2, Application US/09825563
; Patent No. 651228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-09-825-563-2

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAMEVOGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
DB 1 NAMEVOGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
QY 61 DSDYDNDPNDSEMSPCQVQKQOLRQVLRKMLRTSEETISTVQEKQONISPLVERGPQ 120
DB 61 DSDYDNDPNDSEMSPCQVQKQOLRQVLRKMLRTSEETISTVQEKQONISPLVERGPQ 120
QY 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHKG 180
DB 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQOVYIYKTSYPPDILMKSARNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQOVYIYKTSYPPDILMKSARNSCWSKDAEYGLY 240
QY 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHSAFFGAFVLG 281
DB 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHSAFFGAFVLG 281

RESULT 9
US-09-919-039-118
; Sequence 118, Application US/09919039

```
Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaset, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 059509CD1
US-09-919-039-118

Query Match          100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3,5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSDYMDPNDDESMNSPCQWQVKKQLRQLVKRMILRTSEETISTVQEKQONISPLVREGRQ 120
DB 61 DSDYMDPNDDESMNSPCQWQVKKQLRQLVKRMILRTSEETISTVQEKQONISPLVREGRQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKQEKALGRKINSWESSRSGHSFLSLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKQEKALGRKINSWESSRSGHSFLSLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 10
US-09-582-450-1
; Sequence 1, Application US/09582450
; Patent No. 6740739
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Kelley, Robert F.
; APPLICANT: O'Connell, Mark P.
; APPLICANT: Picti, Robert M.
; APPLICANT: Schwall, Ralph H.
; TITLE OF INVENTION: Apo-2 Ligand
; FILE REFERENCE: P0978P4
; CURRENT APPLICATION NUMBER: US/09/582,450
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/007,886
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 09/060,533
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-450-1

Query Match          100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3,5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSDYMDPNDDESMNSPCQWQVKKQLRQLVKRMILRTSEETISTVQEKQONISPLVREGRQ 120
DB 61 DSDYMDPNDDESMNSPCQWQVKKQLRQLVKRMILRTSEETISTVQEKQONISPLVREGRQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKQEKALGRKINSWESSRSGHSFLSLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKQEKALGRKINSWESSRSGHSFLSLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 11
US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. 6746668
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 Ligand
; FILE REFERENCE: 11669,22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match          100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3,5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSDYMDPNDDESMNSPCQWQVKKQLRQLVKRMILRTSEETISTVQEKQONISPLVREGRQ 120
DB 61 DSDYMDPNDDESMNSPCQWQVKKQLRQLVKRMILRTSEETISTVQEKQONISPLVREGRQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKQEKALGRKINSWESSRSGHSFLSLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKQEKALGRKINSWESSRSGHSFLSLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 12
US-10-011-125A-4
; Sequence 4, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
```

;; TITLE OF INVENTION: BACTERIAL HOST STRAINS
;; FILE REFERENCE: P1804R1
;; CURRENT APPLICATION NUMBER: US/10/011,125A
;; CURRENT FILING DATE: 2001-12-07
;; PRIOR APPLICATION NUMBER: US 60/256,162
;; PRIOR FILING DATE: 2000-12-14
;; NUMBER OF SEQ ID NOS: 12
;; SEQ ID NO 4
;; LENGTH: 281
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-011-125A-4

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSDYNDPNDDESMNSPCWQVKMQLRQVVRKMLRTSEETISTVOEKQONISPLVREGRPO 120
DB 61 DSDYNDPNDDESMNSPCWQVKMQLRQVVRKMLRTSEETISTVOEKQONISPLVREGRPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKTSYDPDILMKSAARNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKTSYDPDILMKSAARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 13

PCT-US96-10895-2

; Sequence 2, Application PC/TUS9610895

; GENERAL INFORMATION:

; APPLICANT: Immunex Corporation.

; TITLE OF INVENTION: Cyclokin That Induces Apoptosis

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple 7.5.2

; SOFTWARE: Microsoft Word, Version 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/10895

; FILING DATE: 25-JUN-1996

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/496,632

; FILING DATE: 29-JUN-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/548,368

; FILING DATE: 01-NOV-1995

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Anderson, Kathryn A.

; REGISTRATION NUMBER: 32,172

; REFERENCE/DOCKET NUMBER: 2835-WO

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 587-0430
;; TELEFAX: (206) 233-0644
;; TELEX: 756822
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 281 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match 100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSDYNDPNDDESMNSPCWQVKMQLRQVVRKMLRTSEETISTVOEKQONISPLVREGRPO 120
DB 61 DSDYNDPNDDESMNSPCWQVKMQLRQVVRKMLRTSEETISTVOEKQONISPLVREGRPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKTSYDPDILMKSAARNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKTSYDPDILMKSAARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 14

US-09-072-993C-3

; Sequence 3, Application US/09072993C

; Patent No. 6346388

; GENERAL INFORMATION:

; APPLICANT: Michael R. Brigham-Burke

; APPLICANT: Peter R. Young

; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND

; FILE REFERENCE: CH-50030

; CURRENT APPLICATION NUMBER: US/09/072,993C

; CURRENT FILING DATE: 1998-05-06

; PRIOR APPLICATION NUMBER: 60/055,513

; PRIOR FILING DATE: 1997-08-13

; PRIOR APPLICATION NUMBER: 60/056,980

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/057,550

; PRIOR FILING DATE: 1997-08-29

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 279

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-072-993C-3

Query Match 99.4%; Score 1469; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 3.1e-148;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKEDD 62
DB 1 MMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKEDD 60
QY 63 STWDNDPNDDESMNSPCWQVKMQLRQVVRKMLRTSEETISTVOEKQONISPLVREGRPO 122

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Db      61 SYMDPNDESMNSPCWQVWKQLRQLVRKMLRTSEETISTVOEKQONISPLVREGRQPV 120
QY      123 AAHITGRSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFY 182
Db      121 AAHITGRSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFY 180
QY      183 YIYSQTYFRFOBEIKENTKNDKQWQYIYKTSYPPDPILMKASRNSCWSKDAEYGLYSI 242
Db      181 YIYSQTYFRFOBEIKENTKNDKQWQYIYKTSYPPDPILMKASRNSCWSKDAEYGLYSI 240
QY      243 YOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db      241 YOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 279
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RESULT 15
US-09-569-611C-30
; Sequence 30, Application US/09569611C
; Patent No. 6720182
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-30
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Query Match      83.8%; Score 1238; DB 4; Length 271;
Best Local Similarity 85.4%; Pred. No. 1.3e-123;
Matches 240; Conservative 2; Mismatches 5; Indels 34; Gaps 2;
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QY      61 DDSYMDPNDESMNSPCWQVWKQLRQLVRKMLRTSEETISTVOEKQONISPLVREGRQPV 120
Db      85 DDSYMDPNDESMNSPCWQVWKQLRQLVRK-----KSNKIFLPLVREGRQPV 130
QY      121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
Db      131 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 190
QY      181 FYIYISQTYFRFOBEIKENTKNDKQWQYIYKTSYPPDPILMKASRNSCWSKDAEYGLY 240
Db      191 FYIYISQTYFRFOBEIKENTKNDKQWQYIYKTSYPPDPILMKASRNSCWSKDAEYGLY 250
QY      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db      251 SIYGG-----IDMDHEASFGAFLVG 271
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Search completed: March 2, 2005, 14:52:32
Job time : 52 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 14:47:47 ; Search time 143 Seconds
(without alignments)
644.619 Million cell updates/sec

Title: US-10-077-435-1

Perfect score: 1478
Sequence: 1 MAMMEVGGSPSLGQTCVLIV.....NEHLIDMHGASFGAFLVG 281

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 32804528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing filter 45 summaries

Database : Published Applications AA.*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	8	US-08-916-625B-6
2	1478	100.0	281	8	US-08-921-317A-8
3	1478	100.0	281	9	US-09-813-329-17
4	1478	100.0	281	9	US-09-193-663-8
5	1478	100.0	281	9	US-09-934-465-1
6	1478	100.0	281	10	US-09-919-039-118
7	1478	100.0	281	13	US-10-011-125-4
8	1478	100.0	281	13	US-10-001-054-54
9	1478	100.0	281	14	US-10-093-766-54
10	1478	100.0	281	14	US-10-174-654-11
11	1478	100.0	281	14	US-10-151-882-41
12	1478	100.0	281	14	US-10-218-547-20
13	1478	100.0	281	14	US-10-322-673-72

14	1478	100.0	281	14	US-10-139-785-66	Sequence 66, Appl
15	1478	100.0	281	14	US-10-310-793-26	Sequence 26, Appl
16	1478	100.0	281	15	US-10-279-687-8	Sequence 8, Appl
17	1478	100.0	281	15	US-10-292-486-5	Sequence 5, Appl
18	1478	100.0	281	15	US-10-333-712-1	Sequence 1, Appl
19	1478	100.0	281	15	US-10-662-429-2	Sequence 2, Appl
20	1478	100.0	281	15	US-10-202-062-20	Sequence 20, Appl
21	1478	100.0	281	15	US-10-662-431-2	Sequence 2, Appl
22	1478	100.0	281	15	US-10-662-244-2	Sequence 2, Appl
23	1478	100.0	281	15	US-10-652-242-2	Sequence 2, Appl
24	1478	100.0	281	16	US-10-381-160-5	Sequence 5, Appl
25	1478	100.0	281	16	US-10-755-889-210	Sequence 210, App
26	1478	100.0	281	16	US-10-491-326-1	Sequence 1, Appl
27	1478	100.0	281	17	US-10-771-254-1	Sequence 1, Appl
28	1478	100.0	281	17	US-10-855-559-2	Sequence 2, Appl
29	1469	99.4	279	13	US-10-066-209-3	Sequence 3, Appl
30	1456	98.5	279	16	US-10-367-094-22	Sequence 22, Appl
31	1269.5	85.9	246	9	US-09-855-544A-13	Sequence 13, Appl
32	1017	68.8	208	9	US-09-855-544A-16	Sequence 16, Appl
33	988	66.8	253	15	US-10-652-244-11	Sequence 11, Appl
34	988	66.8	256	15	US-10-652-244-13	Sequence 13, Appl
35	985.5	66.7	461	15	US-10-389-223A-6	Sequence 6, Appl
36	982	66.4	480	15	US-10-389-223A-4	Sequence 4, Appl
37	978	66.2	614	15	US-10-389-223A-2	Sequence 2, Appl
38	964.5	65.3	296	14	US-10-185-425-5	Sequence 5, Appl
39	937.5	63.4	188	9	US-09-855-544A-14	Sequence 14, Appl
40	930	62.9	291	10	US-09-873-829-6	Sequence 6, Appl
41	930	62.9	291	13	US-10-017-910-6	Sequence 6, Appl
42	930	62.9	291	15	US-10-652-244-6	Sequence 6, Appl
43	892.5	60.4	228	17	US-10-855-559-4	Sequence 4, Appl
44	890	60.2	287	16	US-10-367-094-15	Sequence 15, Appl
45	887	60.0	168	9	US-09-900-530A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-916-625B-6
; Sequence 6, Application US/08916625B
; Publication No. US20010010924A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATTNER & PRESTIA
; STREET: P. O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,625B
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/853,684
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/041,230
; FILING DATE: 14-MARCH-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50008-1
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-916-625B-6

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYNDPNDDESMSNPCQOVKQOLRQLVKRMILRTSEETISTVQEKQONISPLVERGPQ 120
DB 61 DDSYNDPNDDESMSNPCQOVKQOLRQLVKRMILRTSEETISTVQEKQONISPLVERGPQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQOVYIYKTSYPPDILLMKSARNSCKDAEYGLY 240
DB 181 FYIYSQTYFRQOEIKENTKNDKQOVYIYKTSYPPDILLMKSARNSCKDAEYGLY 240
QY 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 2

US-08-971-317A-8
Sequence 8, Application US/08971317A
Publication No. US20010010925A1

GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,317A
FILING DATE: 17-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Goller, Mimi C
REGISTRATION NUMBER: 39,046
REFERENCE/DOCKET NUMBER: 6255.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
TELEFAX: (847) 938-2623

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-8

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
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DB 61 DDSYNDPNDDESMSNPCQOVKQOLRQLVKRMILRTSEETISTVQEKQONISPLVERGPQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQOVYIYKTSYPPDILLMKSARNSCKDAEYGLY 240
DB 181 FYIYSQTYFRQOEIKENTKNDKQOVYIYKTSYPPDILLMKSARNSCKDAEYGLY 240
QY 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 3

US-09-813-329-17

Sequence 17, Application US/09813329
Patent No. US20020012968A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 281
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-813-329-17

Query Match 100.0%; Score 1478; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYNDPNDDESMSNPCQOVKQOLRQLVKRMILRTSEETISTVQEKQONISPLVERGPQ 120
DB 61 DDSYNDPNDDESMSNPCQOVKQOLRQLVKRMILRTSEETISTVQEKQONISPLVERGPQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHKG 180
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DB 181 FYIYSQTYFRQOEIKENTKNDKQOVYIYKTSYPPDILLMKSARNSCKDAEYGLY 240

Db. 181 FYIYISQTYFRFOEIKENTKNDKQVQYIYKTYSPDPIILMKASRNSCWSKDAEYGLY 240
QY 241 STYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 STYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 4

US-09-193-663-8
; Sequence 8, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255 US 02
; CURRENT APPLICATION NUMBER: US/09/193,663
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-193-663-8

Query Match 100.0%; Score 1478; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 STYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 STYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 5

US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 Ligand
; FILE REFERENCE: 11669,22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match 100.0%; Score 1478; DB 9; Length 281;

Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKGACFLKE 60
Db 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKGACFLKE 60
QY 61 DSYNDPNDDESMNSPCQVQKQOLVRLVKMLRTSEETISVQEKQONISPLVBERGPQ 120
Db 61 DSYNDPNDDESMNSPCQVQKQOLVRLVKMLRTSEETISVQEKQONISPLVBERGPQ 120
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Db 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVYHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQVQYIYKTYSPDPIILMKASRNSCWSKDAEYGLY 240
Db 181 FYIYISQTYFRFOEIKENTKNDKQVQYIYKTYSPDPIILMKASRNSCWSKDAEYGLY 240
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Db 241 STYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 6

US-09-919-039-118
; Sequence 118, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-118

Query Match 100.0%; Score 1478; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKGACFLKE 60
Db 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKGACFLKE 60
QY 61 DSYNDPNDDESMNSPCQVQKQOLVRLVKMLRTSEETISVQEKQONISPLVBERGPQ 120
Db 61 DSYNDPNDDESMNSPCQVQKQOLVRLVKMLRTSEETISVQEKQONISPLVBERGPQ 120
QY 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVYHEKG 180
Db 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVYHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQVQYIYKTYSPDPIILMKASRNSCWSKDAEYGLY 240
Db 181 FYIYISQTYFRFOEIKENTKNDKQVQYIYKTYSPDPIILMKASRNSCWSKDAEYGLY 240
QY 241 STYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 STYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 7

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US-10-011-125-4
; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125-4

Query Match      100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGGTCVIVITFTVLLQSLCAVATVTVVFTNEMKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGGTCVIVITFTVLLQSLCAVATVTVVFTNEMKQMDKYSKSGIACFLKE 60
QY 61 DSYMDPNDDESMNSPCQVQKMLRQLVAKMLRTSEETISTYQEKQONISPLVERGPO 120
DB 61 DSYMDPNDDESMNSPCQVQKMLRQLVAKMLRTSEETISTYQEKQONISPLVERGPO 120
QY 121 RVAAHITGTRGSNTLSSNSKQEKALGRKINSWESSRSGHSPLSNLHNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSNSKQEKALGRKINSWESSRSGHSPLSNLHNGELVIHEKG 180
QY 181 FYIYSQYFRFQOEIKENTKNDKQVQYIYKTSYPPDILMKARNSCWSKDAEYGLY 240
DB 181 FYIYSQYFRFQOEIKENTKNDKQVQYIYKTSYPPDILMKARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPLAVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPLAVG 281

RESULT 8
US-10-001-054-54
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austrey
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona
; APPLICANT: Shelton, David
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITTING NEOPLASTIC
; TITLE OF INVENTION: CELL GROWTH
; FILE REFERENCE: P3034R1PCT
; CURRENT APPLICATION NUMBER: US/10/001,054
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083545
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088658
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/096891
; PRIOR FILING DATE: 1998-08-17
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; PRIOR APPLICATION NUMBER: 60/100263
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/107783
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112420
; PRIOR FILING DATE: 1998-12-15
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; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116533
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/131294
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/187202
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/209832
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: 09/218517
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 09/284291
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380913
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 09/403297
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/423741
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-08
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PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/866034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/882636
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/924419
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/927796
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: PCT/US98/18824
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/US99/00106
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: PCT/US99/08615
PRIOR FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28634
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00376
PRIOR FILING DATE: 2000-01-06
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/06884
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PCT/US00/13705
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/14941
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/22031
PRIOR FILING DATE: 2000-06-11
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678

PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: PCT/US01/27099
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 54
LENGTH: 281
TYPE: PRT
ORGANISM: Homo Sapien
US-10-001-054-54

Query Match 100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-18;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAMEVQGGPSIGQTCVIVFTVLQSLCAVTVYVTTNEIKQKODKYSKSGIACFLKE 60
DB 1 NAMEVQGGPSIGQTCVIVFTVLQSLCAVTVYVTTNEIKQKODKYSKSGIACFLKE 60
QY 61 DDSYNDPDEBSMNSPCMOVKWQOLVVRKMLRTSEETISVQKQONISPLVERGPQ 120
DB 61 DDSYNDPDEBSMNSPCMOVKWQOLVVRKMLRTSEETISVQKQONISPLVERGPQ 120
QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYYIYSQYFRPQSEIKENTKDKOMVOYIYKTSYPPDILIMKSAARNSCWSKDAEYGLY 240
DB 181 FYYIYSQYFRPQSEIKENTKDKOMVOYIYKTSYPPDILIMKSAARNSCWSKDAEYGLY 240
QY 241 SIYOGIFELKENDRIPIVSUTMEHLIDMDHEASFGALVNG 281
DB 241 SIYOGIFELKENDRIPIVSUTMEHLIDMDHEASFGALVNG 281

RESULT 9
US-10-093-766-54
Sequence 54, Application US/10093766
Publication No. US20030013099A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David A.
TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
FILE REFERENCE: PA-0047 US
CURRENT APPLICATION NUMBER: US/10/093,766
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL Program
SEQ ID NO 54
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54

Query Match 100.0%; Score 1478; DB 14; Length 281;

Best Local Similarity 100.0%; Pred. No. 1.2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCTVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCTVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
Qy 61 DDSYDVPNDEESMNSPCQVQWKQLRQLVRKMIILRTSEETISTVOEKQONISPLVERGPQ 120
Db 61 DDSYDVPNDEESMNSPCQVQWKQLRQLVRKMIILRTSEETISTVOEKQONISPLVERGPQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSNLRLNGELVIHKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSNLRLNGELVIHKG 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPPDILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFVLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFVLVG 281

RESULT 10
US-10-174-654-11

; Sequence 11, Application US/10174654
; Publication No. US20030044937A1

; GENERAL INFORMATION:

; APPLICANT: Bienkowski, Michael J

; Jones, Cynthia J

; TITLE OF INVENTION: TNF-Related Death Ligand

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property

; Legal Services

; STREET: 301 Henrietta Street

; CITY: Kalamazoo

; STATE: MI

; COUNTRY: USA

; ZIP: 49001

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 Diskette

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/10/174,654

; APPLICATION NUMBER: US/10/174,654

; FILING DATE: 19-Jun-2002

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Kerber, Lori L.

; REGISTRATION NUMBER: 41,113

; REFERENCE/DOCKET NUMBER: 6111.N CNI

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 616/833-0974

; TELEFAX: 616/833-8897

; TELEX: 224401

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 281 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-174-654-11

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCTVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCTVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
Qy 61 DDSYDVPNDEESMNSPCQVQWKQLRQLVRKMIILRTSEETISTVOEKQONISPLVERGPQ 120
Db 61 DDSYDVPNDEESMNSPCQVQWKQLRQLVRKMIILRTSEETISTVOEKQONISPLVERGPQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSNLRLNGELVIHKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSNLRLNGELVIHKG 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPPDILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFVLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFVLVG 281

RESULT 11
US-10-151-882-41

; Sequence 41, Application US/10151882
; Publication No. US20030039862A1

; GENERAL INFORMATION:

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)

; FILE REFERENCE: PF554

; CURRENT APPLICATION NUMBER: US/10/151,882

; PRIOR FILING DATE: 2002-05-22

; PRIOR APPLICATION NUMBER: 60/293,100

; PRIOR FILING DATE: 2001-05-24

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: Patentin version 3.0

; SEQ ID NO: 41

; LENGTH: 281

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-151-882-41

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCTVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCTVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
Qy 61 DDSYDVPNDEESMNSPCQVQWKQLRQLVRKMIILRTSEETISTVOEKQONISPLVERGPQ 120
Db 61 DDSYDVPNDEESMNSPCQVQWKQLRQLVRKMIILRTSEETISTVOEKQONISPLVERGPQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSNLRLNGELVIHKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSNLRLNGELVIHKG 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPPDILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFVLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFVLVG 281

RESULT 12
US-10-218-547-20

; Sequence 20, Application US/10218547
; Publication No. US20030100074A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel

```

; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-218-547-20
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Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MAMMEVQGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNI SPLVERGPQ 120
DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNI SPLVERGPQ 120
QY 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRNGLVIHKG 180
DB 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRNGLVIHKG 180
QY 181 FYYISQTFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEYGLY 240
DB 181 FYYISQTFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRI FVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRI FVSVTNEHLIDMDHEASFGAFLVG 281
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```

RESULT 13
US-10-322-673-72
; Sequence 72, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF565
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-72
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Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-128;
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Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNI SPLVERGPQ 120
DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNI SPLVERGPQ 120
QY 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRNGLVIHKG 180
DB 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRNGLVIHKG 180
QY 181 FYYISQTFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEYGLY 240
DB 181 FYYISQTFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRI FVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRI FVSVTNEHLIDMDHEASFGAFLVG 281
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RESULT 14
US-10-139-785-66
; Sequence 66, Application US/1039785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-66
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Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MAMMEVQGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNI SPLVERGPQ 120
DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNI SPLVERGPQ 120
QY 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRNGLVIHKG 180
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Db      121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSPFLNHLIRNGELVIHEKG 180
Qy      181 FYIYSQTYFRPOEBIKENTKNDKOMVOYIYKYTSYDPDILMKSARNSCSKDAEYGLY 240
Db      181 FYIYSQTYFRPOEBIKENTKNDKOMVOYIYKYTSYDPDILMKSARNSCSKDAEYGLY 240
Qy      241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db      241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 15
US-10-310-793-26
; Sequence 26, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; FILE REFERENCE: P573
; CURRENT FILING DATE: 2002-12-06
; PRIOR FILING DATE: 2002-12-06
; PRIOR FILING DATE: 2001-12-07
; PRIOR FILING DATE: 2002-08-23
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2001-07-06
; PRIOR FILING DATE: 2001-07-06
; PRIOR FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-02-08
; PRIOR FILING DATE: 1999-05-13
; PRIOR FILING DATE: 1999-05-13
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-310-793-26

Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NAMEVQGGPSLGGTCVLIVITVLLQSLCAVATYYFPTNELKOMODKYSKGIACFLKE 60
Db      1 NAMEVQGGPSLGGTCVLIVITVLLQSLCAVATYYFPTNELKOMODKYSKGIACFLKE 60
Qy      61 DSYNDPNDSESMNSPCWQVKQLRQLVKMTLRTSEETISTVOEKQONISPLVREGRPO 120
Db      61 DSYNDPNDSESMNSPCWQVKQLRQLVKMTLRTSEETISTVOEKQONISPLVREGRPO 120
Qy      121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSPFLNHLIRNGELVIHEKG 180
Db      121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSPFLNHLIRNGELVIHEKG 180
Qy      181 FYIYSQTYFRPOEBIKENTKNDKOMVOYIYKYTSYDPDILMKSARNSCSKDAEYGLY 240
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Db      181 FYIYSQTYFRPOEBIKENTKNDKOMVOYIYKYTSYDPDILMKSARNSCSKDAEYGLY 240
Qy      241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db      241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
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Search completed: March 2, 2005, 15:03:07
Job time : 144 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 14:40:57 ; Search time 48 seconds
(without alignments)
563.269 Million cell updates/sec

Title: US-10-077-435-1
Perfect score: 1478
Sequence: 1 MAMMEVQGSFSLGQTCLIV.....NEHLIDMDHEASFGAFVLVG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189.5	12.8	279	2 A53062	Fas ligand - mouse
2	186	12.6	281	2 I38707	Fas ligand - human
3	177.5	12.0	278	2 A49266	Fas ligand - rat
4	164	11.1	261	2 S53090	CD40 ligand - bovi
5	147.5	10.0	261	2 I53476	CD40 ligand - huma
6	141	9.5	234	1 A25451	tumor necrosis fac
7	141	9.5	260	2 S21738	CD40 ligand - mous
8	134.5	9.1	204	1 S17289	tumor necrosis fac
9	133	9.0	232	1 S12606	tumor necrosis fac
10	131.5	8.9	233	1 S22052	tumor necrosis fac
11	131	8.9	234	1 J01344	tumor necrosis fac
12	130.5	8.8	233	1 S24642	tumor necrosis fac
13	129.5	8.8	235	1 I54490	tumor necrosis fac
14	127.5	8.6	204	1 S24641	lymphotoxin - bovi
15	125.5	8.5	233	1 QMHUN	tumor necrosis fac
16	123.5	8.4	235	1 QMHUN	tumor necrosis fac
17	123.5	8.4	235	2 J00029	tumor necrosis fac
18	122	8.3	205	1 QMHUX	lymphotoxin alpha
19	121	8.2	234	1 JH0529	tumor necrosis fac
20	115.5	7.8	193	2 S06192	tumor necrosis fac
21	114	7.7	202	1 B27303	tumor necrosis fac
22	113.5	7.7	185	2 S52715	tumor necrosis fac
23	113.5	7.7	306	2 I49139	lymphotoxin-beta -
24	112.5	7.6	638	1 QCBY2M	mRNA meturase b14
25	111.5	7.5	202	1 JN0869	tumor necrosis fac
26	109	7.4	652	2 I48083	amphotropic murine
27	107	7.2	197	1 JH0309	tumor necrosis fac
28	102	6.9	244	2 A46066	lymphotoxin beta -
29	100	6.8	865	2 AB1658	probable membrane

30	99.5	6.7	233	2 S11688	tumor necrosis fac
31	97.5	6.6	448	2 P5122	protein kinase, pr
32	95	6.4	345	2 T14707	DNA ligase homolog
33	95	6.4	365	2 T15010	hypothetical prote
34	95	6.4	455	2 G95104	hypothetical prote
35	94.5	6.4	4981	2 T18489	hypothetical prote
36	94	6.4	1465	2 T23056	chromodomain helic
37	92.5	6.3	833	1 A31593	heat shock transcr
38	92.5	6.3	1538	2 T29095	cardiac muscle fac
39	91	6.2	1176	2 JN0583	myosin-light-chain
40	90.5	6.1	502	2 UC2491	serine/threonine k
41	90.5	6.1	502	2 A53444	activin receptor-1
42	90.5	6.1	1284	2 T40578	hypothetical prote
43	90	6.1	907	2 E9636	hypothetical prote
44	89.5	6.1	313	2 T03031	NBS-LRR type resis
45	89	6.0	328	2 B59296	alpha-N-arabino fur

ALIGNMENTS

```
RESULT 1
A53062
Fas ligand - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: A53062
R:Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A>Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A:Reference number: A53062; MUID:94185175; PMID:7511063
A:Accession: A53062
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-279 <TAK>
A:Cross-references: UNIPROT:P41047; GB:U06948; NID:9473564; PIDN:AA17800.1; PID:9473565

Query Match
Query Local Similarity 12.8% Score 189.5; DB 2; Length 279;
Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;

QY 83 QLRQLVRKMLRTSETISTVQEKQONISPLVREGRPVVAHITGRGSRNTLSSPSNK 142
DB 111 ELREFTNGSL-----KVSSEKQIANPSTSEKKEPRSV-AHLG-----NPSHR 154

QY 143 NEKALGRKINWESRSGHFLSNLHNGELVHKEGPYYISQTYRFRPEIKENTKN 202
DB 155 SIPL-----EWEDT-YGTALISGVKKKGGLVNETGLVFPVSKYFRGQ-----SCN 201

QY 203 DKQWQYIY-KTYSYDPDILMLKSAR-NSCWSKDAEYGLYSYGIGIFELKENDRIFVS 260
DB 202 NQPLNHKVMKRSKYPEDLVLMERKLVYCTT--CQIWAHSSYLGAENLISADHLVNI 259

QY 261 TNEHLIDMDHEASFGAF 278
DB 260 SGLSLINFEBSKTFRGV 277

RESULT 2
138707
Fas ligand - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: 138707; J02340; S57565; 138534
R:Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A>Title: Human Fas ligand: gene structure, chromosomal location and species specificity.
A:Reference number: 138707; MUID:95127560; PMID:7826947
A:Accession: 138707
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-281 <RES>
A:Cross-references: UNIPROT:P48023; EMBL:U11821; NID:9595430; PIDN:AA50124.1; PID:959541
```


R.Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A>Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A'Reference number: JG2340; MUID:95071350; PMID:7980902
A'Accession: JG2340
A'Molecule type: DNA
A'Residuals: 1-281 <MIT>
A'Cross-References: GB:D38122; DDBJ:D29820; NID:G601892; PIDN:BA07320.1; PID:G1369902
R.Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A'Reference number: S57565
A'Accession: S57565
A'Status: preliminary
A'Molecule type: mRNA
A'Residuals: 1-281 <SCH>
A'Cross-References: EMBL:X89102; NID:G987455; PID:G987456
R.Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G.C. J. Exp. Med. 181, 71-77, 1995
A>Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A'Reference number: 138554; MUID:95105731; PMID:7528780
A'Accession: 138554
A'Status: preliminary; translated from GB/EMBL/DDBJ
A'Molecule type: mRNA
A'Residuals: 1-281 <RE2>
A'Cross-References: EMBL:U08137; NID:G624627; PIDN:AAC50071.1; PID:G624628
C'Genetics:
A'Gene: FasL
A'Introns: 151/1; 116/3
C'Keywords: glycoprotein; transmembrane protein
F180-102/Domain: transmembrane #status predicted <TM>
F176,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 186; DB 2; Length 281;
Best Local Similarity 12.1%; Pred. No. 3.4e-08;
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

QY 4 MEVGGPSIGQTCVLIIVFTLLQSLCAVAV--TYVYFTNELKQMDKYSKSGIACFLKE 60
DB 71 LKRRGNHSTG-LCLVMPFVVLVALVGLGFMFOLFHLOKELAEIRESTSQMHTASLSEK 129
QY 61 DSYNDPNDDESMNSPCQVKKQLQVLRKMLRTSEERTISTVQEQQINISPLVNERGQ 120
DB 130 QIGHSPPE-----KKELRV----- 146
QY 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSMESSRGHSLNHLRNGELVYHEK 180
DB 147 ---ALIT---GKSNRSNP-----LEWEDT-XGIVLSGVKTKGGLVINEIG 187
QY 181 FYIYISQTYFRFOEIKENTKDKQVQYIY-KYTSYDPDILMKSAANS-----CWSK 233
DB 188 LYFVYSKYVFRGQ-----SCNNLPLSHKVVYRNSKYPODLVMEGKKMSYCTTGQMMAR 241
QY 234 DAEYGLYSTYGGIFELKENDRIFFVSYVNEHLIDMDHEASFGAR 278
DB 242 -----SSYLGAVFNLTSADHLVYVNSLSLVNFEESQTFGLY 279

RESULT 3
A49266
fas ligand - rat
C'Species: Rattus norvegicus (Norway rat)
C'Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C'Accession: A49266
R.Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A>Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
A'Reference number: A49266; MUID:94084792; PMID:7505205
A'Accession: A49266
A'Status: preliminary
A'Molecule type: mRNA
A'Residuals: 1-278 <SD>
A'Cross-References: UNIPROT:P36940; GB:U03470; NID:G440178; PIDN:AAC52129.1; PID:G440178
C'Keywords: glycoprotein; transmembrane protein

Query Match 12.0%; Score 177.5; DB 2; Length 278;
Best Local Similarity 12.5%; Pred. No. 1.8e-07;
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

QY 100 ISTVQKQONISPLVBERGQVAAHITG-GRGNTLSSPNSKNEKALGRKINSMESSR 158
DB 121 VSSFEKQJANSTPSETKKPRSV-AHLGNPNSRSIPL-----EWEDT- 162
QY 159 SGHSFLSNLHLRNGELVHERGFFYISQTYFRFOEIKENTKDKQVQYIY-KYTSY 217
DB 163 YGTALISGVKTKGGLVINEGLVYVSKVIFRGQ-----SCNSQPSHKVYKFNKYP 216
QY 218 DFIILKKSAR-NSCWSKDAEYGLYSIYGGIFELKENDRIFFVSYVNEHLIDMDHEASFG 276
DB 217 GDVLVMEKKINCYCT--GQIWAHSSYLGAVFNLVADHLVYVNSQLSILNFEESKTFRG 274
QY 277 AF 278
DB 275 LY 276

RESULT 4
S53090
CD40 ligand - bovine
C'Species: Bos primigenius taurus (cattle)
C'Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C'Accession: S53090
R.Mertens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A'Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A'Reference number: S53090
A'Accession: S53090
A'Status: preliminary
A'Molecule type: mRNA
A'Residuals: 1-261 <MER>
A'Cross-References: UNIPROT:P51749; EMBL:Z48469; NID:G732569; PIDN:CAA88363.1; PID:G7325

Query Match 11.1%; Score 164; DB 2; Length 261;
Best Local Similarity 25.9%; Pred. No. 2.3e-06;
Matches 72; Conservative 52; Mismatches 114; Indels 40; Gaps 14;

QY 6 VGGPSLQOTCVLIIVFTLL--QSLCAVAVTYVFTNELKQMDKYSKSGIACFLKEDDS 63
DB 13 VATGPVPMK-IFMYLLVFLITQWIGSALFVYVLRDLKIEDERNLHEDVFMK--T 68
QY 64 YMDPNDDESMNS--PCQVKKQLQVLRKMLRTSEERTISTVQEQQINISPLVNERGQ 121
DB 69 IQRCKRGGSLSLNCBEIRGRFEDLV-KDLMQNR-----VKKEKPEMHKGDQEPQ- 121
QY 122 VAAHITGRGNTLSSPNSKNEKALGRKINSMESSRGHSLN--LHLRNG-ELVYHE 178
DB 122 IAAHV-----ISEASSKTTSL-----QW-APKGYITLSNNLVTLNKGKGLAVKR 165
QY 179 KGFYIYISQTYFRFOEIKENTKDKQVQYIYKYTSYDPDILMKSAANSWSKDAEYG 238
DB 166 GGFYIYIYQVFCNSNR-----TLGAPPIASLCLSPGSEIRILLRANHTSSSRPC--G 219
QY 239 LYSIYGGIFELKENDRIFFVSYVNEHLIDMDHEASFG 276
DB 220 QQSILHGVFELQSGAVFVAVTDPDSQVSHGTGTFSG 257

RESULT 5
I53476
CD40 ligand - human
N'Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C'Species: Homo sapiens (man)
C'Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C'Accession: I53476; JH0793; S26594; S28852; I53476; S25684; S30593
R.Hollenbaugh, D.; Grosmaire, L.S.; Kullaa, C.D.; Chalupny, N.J.; Breesch-Andersen, S.;
EMBO J. 11, 4313-4321, 1992
A>Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for

A:Reference number: S28017; MUID:93049181; PMID:1385114
A:Accession: S28017
A:Molecule type: mRNA
A:Residues: 1-261 <HOU>
A:Cross-references: UNIPROT:p29695; EMBL:Z15017; NID:g38483; PIDN:CAA78737.1; PID:g38484
R:Exp. 1999, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
J. Exp. Med. 176, 1543-1550, 1992
A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin
A:Reference number: JH0793; MUID:93094757; PMID:1281209
A:Accession: JH0793
A:Molecule type: mRNA
A:Residues: 1-261 <SPR>
A:Cross-references: GB:X67878; NID:g38411; PIDN:CAA8077.1; PID:g38412
A:Experimental source: peripheral blood T-cell
R:Grif, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroccek, R.A.
Eur. J. Immunol. 22, 3191-3194, 1992
A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A:Reference number: S26694; MUID:93076854; PMID:1280226
A:Accession: S26694
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <GRA>
A:Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA6554.1; PID:g37270
R:Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Lile, P.; Tomotte, T.; Elson, G.; Bonnefoy, J.
FEBS Lett. 315, 259-266, 1993
A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e
A:Reference number: S28852; MUID:93138085; PMID:7678552
A:Accession: S28852
A:Molecule type: mRNA
A:Residues: 1-261 <GAU>
A:Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA55667.1; PID:g180124
A:Note: The sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
A:Genetics:
A:Gene: GDB:CD40LG; HIGM1; IMD3
A:Cross-references: GDB:120632; OMIM:308230
A:Map position: Xq26-Xq26
C:Keywords: glycoprotein; transmembrane protein
F:13-44/Domain: transmembrane #status predicted <TM>
F:45-261/Domain: extracellular #status predicted <EXT>
F:6-240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	10.0%	Score 147.5	DB 2	Length 261
Best local Similarity	23.7%	Pred. No. 5.7e-05		
Matches	66	Conservative 51	Mismatches 99	Indels 63
			Gaps 15	
QY	17	VLIVFTYLL--QSLCAVAVTVYFTNELKQMODKYSKGIACFLKEDSDYMDP-----ND	69	
DB	23	IFWLLITVFLITOMGSLFAVYLLHRDLKIEDEN-----LHEDVVPKKTORCNTG	75	
QY	70	ESNN--SPQVQWQRLQRLVRKMLIRTSSEETISVQEKQONISPLVRGRGQVAAHITG	128	
DB	76	ERSLILNCEIKSQPEGFVMDIML-NKEET-----KKNSEPMQKQDNPQ-IAAHV--	126	
QY	129	TRGRNNTLSSPNSKKEKALGRKINWESSRSGHSLN--LHRLRG-ELVHEKGFYIY	185	
DB	127	-----ISEASSKITSVL-----QW--AEKGYTMSNLLVLENGKOLTYRKQGLYYIY	172	
QY	186	SQTVRFPQBEIKENT-----KNDKQWQVQIYKYTSYPPILMKSGARNSCSKDAEY	237	
DB	173	AOVTCNSRNKASSQAPFLASLCLKSPGRFR-----ILRLAANTHSSAKPC--	218	
QY	238	GLYSIVQIGIFELKENDRIFVSVTNEHLIDMDHEASFFG	276	
DB	219	GGQSIHLGSGVFLQPGASVFVNVVTDPSQVSHOTGTSFG	257	

RESULT 6
A25451
tumor necrosis factor alpha precursor - rabbit
N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C:Accession: A25454; A25451; J050727

RiTo, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.
 RNA 5, 149-156, 1986
 A>Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for, rat
 A:Reference number: A25454; MUID:66219711; PMID:3519137
 A:Accession: A25454
 A:Molecule type: mRNA
 A:Residues: 1-234 <IT0>
 A:Cross-references: UNIPROT:P04924; GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
 RiTo, H.; Shirai, T.; Yamamoto, S.; Akita, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
 DNA 5, 157-165, 1986
 A>Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
 A:Reference number: A25451; MUID:66219712; PMID:3519138
 A:Accession: A25451
 A:Molecule type: DNA
 A:Residues: 1-234 <IT2>
 A>Note: this sequence differs from that shown in having a Gln inserted between residues
 R,Shikhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
 Gene 95, 215-221, 1990
 A>Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF
 A:Reference number: JH0309; MUID:91065534; PMID:2249779
 A:Accession: J50727
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-62, 'Q', 63-234 <SHA>
 A:Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
 C:Genetic8:
 A:Introns: 62/3; 80/1; 96/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cyclooxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
 F:1-81/Domain: propeptide #status predicted <PRO>
 F:82-234/Product: tumor necrosis factor #status predicted <MAT>
 F:19,20/Binding site: myristate (lys) (covalent) #status predicted
 F:83/Binding site: carbonylate (Ser) (covalent) #status predicted
 F:147-178/Dissulfide bonds: #status predicted

Query Match 9.5%; Score 141; DB 1; Length 234;
 Best Local Similarity 22.4%; Pred. No. 0.00017;
 Matches 62; Conservative 41; Mismatches 98; Indels 76; Gaps 13;

Oy	8	GGPSLQGTCLVLIIVITVLLQSLCAVATVTVVFTNELKQMODKYSKSGIACFLKEDDSYWP	67
Db	22	GGPGSKRCICLISLFSFL-----VAGATTLF-----CLL--HFRVIGP	58
Oy	68	NDEESKNSPCMQVKQKQLRQLVRKMI-LRTSEBITSTVQEKQONISPLVREBGFQVAAH	126
Db	59	QEEBSPPNN-----LHLVNPVACQVTLRSASRALSD-----KPL-----AHV	94
Oy	127	TGTRGRNTLSSPNSKNEKQLGRKINWESRSCHSLNHLRNGELVTHEKGFYYIS	186
Db	95	VA-----NPVEGQL-----QWLSQRAAALIANQKCLTDNLVVPADGLYIIS	138
Oy	187	QTYRPOEIKENTKNQKQWQVYIKY-TSYPDPIILMKASNSCKSDAEYG-----LY	240
Db	139	QVLFESGQ-----GGRSVLLTHYTRSPAVSEYKNNVNLSSIKSCHHETFEBAEMPMAYE	193
Oy	241	SIYQGIPELKENDRIFVSVTNEHLIDMDHEAS-FFG	276
Db	194	PVILGVFQLEKGRDLSTEVNQPEYLDLAESQVYFG	230

RESULT 7
 S21738
 CD40 ligand - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: S21738
 R:Armstrong, R.J.; Farnlow, W.C.; Strockbine, L.; Seto, T.A.; Clifford, K.N.; Machuga, B.
 Nature 357, 80-82, 1992
 A>Title: Molecular and biological characterization of a murine ligand for CD40.
 A:Reference number: S21738; MUID:92244364; PMID:1374165
 A:Molecule type: mRNA

Db 182 EGAERAPWEPYILGVFQLEKODRLSAEINLPDYLDPAESGQVYFG 228

RESULT 10
S22052
tumor necrosis factor alpha precursor - baboon
C.Species: Papio sp. (baboon)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: S22052
R.Sanjana, W.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A.Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A.Reference number: S22052
A.Accession: S22052
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-233 <SAN>
A.Cross-references: UNIPROT:P33620; EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g378160
C.Gene: TNF-alpha
A.Introns: 62/3; 78/1; 94/1
C.Superfamily: tumor necrosis factor
C.Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
P.19_20/Binding site: myristate (lys) (covalent) #status predicted
F.81/Binding site: carbohydrate (Ser) (covalent) #status predicted
P.145-177/Disulfide bonds: #status predicted

Query Match 8.9%; Score 131.5; DB 1; Length 233;
Best Local Similarity 19.2%; Pred. No. 0.0011;
Matches 55; Conservative 49; Mismatches 98; Indels 85; Gaps 10;

Qy 2 AMMEVGGSPLSGQTCLIVFTVLQSICAVTYVTFNELKOMQDKSKGIACFLKED 61
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 16 ALPKKGPGSPGRCLPLSFSLVLAATTLFCLLHFGVIGIQPOBEFPK----- 65
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 62 DSWMDTNDSESNKSPQCQVMQLQLRVKMILTSTSEITISTYGEKQNISPLYRERGPR 121
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 66 ----DP----SLISPLQA-----VRSSSRPS-----DK 87
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 122 VAHITGTGRSNTLSPPNSKNRKALGRKINSMESSRSQHSFLSMHLNLNGELVIHEKGF 181
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 88 PVAHVVA-----NQAEGL--QMNRRAANALLANGVELRADNQLVPSEGL 131
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 182 YIYSQTYPFQOEIKENTKDKOMVOYIYKT-----SYDPIILMKASRNCSMK-- 233
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 132 YLIYSQVLFKGO-----GCPTHYLTHTTSIRIAVSYTQKVNLISAISKPCORETP 182
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 234 ---DAEVGLXSIYOGGIFELKENDRIFVSVTNEHLIDMDEMS-FRG 276
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 183 EGAEARPWEPYILGVFQLEKGRDLASAINLPDYLDPAESGQVYFG 229

RESULT 11
JOL344
tumor necrosis factor alpha precursor - horse
N.Alternate names: cachectin; TNF alpha
C.Species: Equus caballus (domestic horse)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: JOL344
R.Su, X.J. Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
Article: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f
A.Reference number: JOL344; MUID:92084125; PMID:1748301
A.Accession: JOL344
A.Molecule type: DNA
A.Residues: 1-234 <SU>
A.Cross-references: UNIPROT:P29553; GB:M6087; NID:g164244; PIDN:AAA30959.1; PID:g164245
C.Comment: This protein is an important proximal mediator of endotoxemia.
C.Gene: TNF-alpha
A.Introns: 62/3; 79/1; 95/1
C.Superfamily: tumor necrosis factor
C.Keywords: cytokine; cytotoxic; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F.78-734/Product: tumor necrosis factor alpha #status predicted <TM>

F.19/20/Binding site: myristate (Lys) (covalent) #status predicted
 F.82/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F.146-178/Dienulfide bonds: #status predicted

```

Query Match          8.9%; Score 131; DB 1; Length 234;
Best Local Similarity 20.8%; Pred. No. 0.0012;
Matches 60; Conservative 40; Mismatches 89; Indels 100; Gaps 13;

QY 8 GGPSSGQTVLIVIFVVLQSLCAVATVYVFTNELKQMDKXKSGIACFL-----K 59
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 22 GPOGSRRLCTLSLFSFLL-----VAGATTLF-----CLLHFVIGPQR 60
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 60 BDDSYWMDPDESNMSPCMQVWKQLRQLVRKMLRTSEETISTVQEKQONISPLRERGP 119
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 61 EEQL---PNAFOSIN-PLAQT-----LRSSRTPS-----86
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 120 QVAAHITTRRSNTLSSPNSKNEKALGRKINSWESSRGHSEFLSNLHNGELVIEHK 179
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 87 DKPVAHVVA-----NPAEGL---QWLSGRANALLANGVKLLDNGLVVPLD 130
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 180 GFYIYVSYQTFPRPQEEIKENTKNDKQMVQIYYT-----SYDDPILMKSNRSCSK 233
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 131 GLYLIYSQVLFKQ-----GCPSTHVLTHTISRILAVSYSPKVLNLAIKSPCHTE 181
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 234 DAHYG-----LYSIYGGIFELKENDRIFVSVNHEHIDMDEMS-PRG 276
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 182 SPEQAEAKWPEPIYGVGFQELGQQLSAEINQPNYLDFAESGQVYFG 230
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 12
S24642
tumor necrosis factor alpha precursor - bovine
CISpecies: Bos primigenius taurus (cattle)
CDate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
CAccession: I46047; S24642
RClndrs: I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Dooogmans, L.
CytoKine 5, 336-341, 1993
AtTitle: Cloning and characterization of the tandemly arranged bovine lymphotoxin and
AReference number: I46046; MUID:94083525; PMID:8260599
AAccession: I46047
AStatus: preliminary; translated from GB/EMBL/DBJ
AMolecule type: DNA
AResidues: 1-233 <CL2>
ACross-References: UNIPROT:Q06599; EMBL:Z14137; NID:9796; PIDN:CAA78511.1; PID:g798
C:Genetics
A:Gene: TNFA
A:Introns: 62/3; 78/1; 94/1
CISuperfamily: tumor necrosis factor
CKeywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F.120/Binding site: myristate (Lys) (covalent) #status predicted
F.81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F.145-177/Dienulfide bonds: #status predicted

Query Match          8.8%; Score 130.5; DB 1; Length 233;
Best Local Similarity 20.3%; Pred. No. 0.0013;
Matches 59; Conservative 43; Mismatches 95; Indels 93; Gaps 13;

QY 3 MMEVGGSPISGQTVLIVIFVVLQSLCAVATVYVFTNELKQMDKXKSGIACFL----- 58
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 17 LSEKKGSGPQSSRSLCLSLFSFLL-----VAGATTLF-----CLLHFGV 55
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 59 ---KEDSYWMDPDESNMSPCMQVWKQLRQLVRKMLRTSEETISTVQEKQONISPLVR 115
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 56 IGPRSEESPGP---SINSPVQT-----LRSSQAS-----85
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 116 ERGPRVAAHITGTRKRSNTLSSPNSKNEKALGRKINSWESSRGHSEFLSNLHNGELV 175
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 86 ---NKPVAHVVA-----DINSFGQLR-----MWDSYANALMANGVKLEDNQLV 125
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 176 IHEKGFYIYVSYQTFPRPQEEIKENTKNDKQMVQIYK---YTSYDPDILMKSNRSC--- 230
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 126 VPADGLYLIYSQVLFKQ-----GCPSTPLFTHTISRILAVSYQTKVNITLAIKSPCHRE 180
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
  
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Oy 231 ---MSKDAEGLYSYOGGIFELKENDEIPFVSVTNEHLIMDHEAS -FPG 276
 |::||::|::|::|::|::|::|::|::|::|::|:
Db TPBWA-EAKPWYEPIYGQGVFOLEKGDRLSAEINLPDIYLDAESGGVTFG 229

RESULT 13
154490
tumor necrosis factor alpha precursor - white-footed mouse
C:Species: Peromyscus leucopus (white-footed mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I54490
R:Crew, M.D.; Filipowaky, M.E.
Immunogenetics 35, 351-353, 1992
A>Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus
A:Reference number: I54490; MUID:92218012; PMID:11348497
A:Accession: I54490
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: UNIPROT:P36939; GB:M59233; NID:g202506; PIDN:A440596.1; PID:g202507
C:Genetics:
A:Gene: PNTNF
A:introns: 62/3; 81/1; 97/1
C:Superfamily: tumor necrosis factor
C:keywords: glycoprotein; lipoprotein; myristylation
F:19/20/Binding site: myristate (Lys) (covalent) #status predicted
F:84/Binding site: carbonydrate (Ser) (covalent) #status predicted

Query Match 8.8%; Score 129.5; DB 2; Length 235;
Best Local Similarity 24.5%; Pred. No. 0.0016;
Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;

Oy 110 ISPLVRERGPORVAAHITGTGRSNTLSSPNSKNKEALGRKINSWE-----SSRSQH 161
 |::||::|::|::|::|::|::|::|::|::|::|:
Db IGPOREEKFNNLP--IIGSMAGQTILRSSQSNDSPKAHVAVNHQVDQLFWLSRGAN 113

Oy 162 SFLSN-LHRLNGELVIHKGFYYISQTYFRFFOEIKENTKDQMGOYIYKY-TSPDP 219
 |::|::|::|::|::|::|::|::|::|::|::|:
Db ALLANGMDLKNOATLLPADGLLYLVSOVLPRFGQ----GCSSYVALTHHTVASFAVSIEDK 168

Oy 220 ILMKARSANCWSDAEGX-----LVSIYGGIFELKENDRIPFVSVTNEHLIMDHEAS 273
 |::|::|::|::|::|::|::|::|::|::|::|:
Db VNLSAIKSPP-KPETPEGSSELKPWEPITYLGCVFOLEKGDRLSAEVNLPKIYLDPAESQG 227

Oy 274 -FPG 276
 |::||
Db DDBS 228 VYFG 231

RESULT 14
S24641
lymphotoxin - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: T46046; S24641
R:Cludat, L.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A>Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and cytokines
A:Reference number: T46046; MUID:94083525; PMID:8260599
A:Accession: T46046
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-204 <CLT>
A:Cross-references: UNIPROT:Q06600; EMBL:T14137; NID:g796; PIDN:CAA78510.1; PID:g797
C:Genetics:
A:introns: 32/3; 68/1
C:Superfamily: tumor necrosis factor

Query Match 8.6%; Score 127.5; DB 1; Length 204;
Best Local Similarity 24.9%; Pred. No. 0.002;
Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

Oy 99 TISTVQEKOONISPLVRERGFORVAHAHTG-----TRGSNTLSSPNSKNKEALGRKI 151

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Db      40  TP$AAQ$AAHQOL-PTPTRTGTLKPAALVVD$P$QD$LR$RAT-----DRAFLR-- 88
Oy      152  NSW$SS$SGH$PSL$NLH$RNGELV$HEKGFYIYSQTF$P$Q$BEIK$ENTK$DK$OM$VOYIY 211
Db      89  -----HG$F-----SL$N$N$SL$VPT$SG$YGFVYSQV$F$G$R$G$CF$P$RAT$P$PL$YLA$EVQ 135
Oy      212  KYT-$SY$D$P$LL$MKS$A$N$SC$M$K$D$A$E$G$Y$S$IY$Q$G$I$F$E$K$END$R$I$V$S$V$T$N-$E$H$L$D$M$D 269
Db      136  L$F$Q$Y$F$H$V$P$LL$S$AQ$K$V$C$P$G$P$W-$V$S$V$Q$A$V$F$LL$TR$D$Q$U$S$T$H$D$G$I$SH$L$-L$S 193
Oy      270  HEA$F$F$G$A$F 278
Db      194  P$S$V$F$F$G$A$F 202

RESULT 15
OMHUN
tumor necrosis factor alpha precursor [validated] - human
N/Alternate names: cachectin; TNFA
C/Species: Homo sapiens (man)
C/Date: 28-Aug-1985 #sequence, revision 28-Aug-1985 #text, change 09-Jul-2004
C/Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B233
P/Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.;
Nucleic Acids Res. 13, 6361-6373, 1985
A/Title: Human lymphokinin and tumor necrosis factor genes: structure, homology and chrc
A/Reference number: A93585; MUID:86016093; PMID:2995927
A/Accession: A93585
A/Molecule type: DNA
A/Residues: 1-233 <NED>
A/Cross-references: UNIPROT:P01375; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; P
R/Ittis, F.O.M.; Bougueleret, L.; Priour, S.; Caterina, D.; Primas, G.; Petroc, V.; Jurkac
Nature Genet. 3, 137-145, 1993
A/Title: Dense Ali clustering and a potential new member of the NFkappaB family within a
A/Reference number: S36153; MUID:93272029; PMID:8499947
A/Accession: S36153
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-233 <IRI>
A/Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
A/Note: this protein was isolated from the monocytic-like cell line HL-60 from a promyeloc
R/Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature 312, 724-729, 1984
A/Title: Human tumour necrosis factor: precursor structure, expression and homology to 1
A/Reference number: A93351; MUID:85086244; PMID:6392892
A/Accession: A93351
A/Molecule type: mRNA
A/Residues: 1-233 <PEN>
A/Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A/Note: this protein was isolated from the monocytic-like cell line HL-60 from a promyeloc
R/Mang, A.M.; Creesey, A.A.; Ladner, M.B.; Lin, L.S.; Stickler, J.; Van Arsdel, J.N.;
Science 228, 149-154, 1985
A/Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A/Reference number: A44189; MUID:85142190; PMID:3856324
A/Accession: A44189
A/Molecule type: mRNA
A/Residues: 1-62, 'S', '64'-233 <MAN>
A/Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
R/Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; And
Lymphokine Res. 7, 175-185, 1998
A/Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A/Reference number: A61478; MUID:88301617; PMID:2841543
A/Accession: B61478
A/Molecule type: protein
A/Residues: 83-102,109-119,121-128, 'X',130-131,142-144, 'X',146, 'XXX',150-152,159-174,180
R/Mamenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Biochem. 152, 515-522, 1995
A/Title: Molecular cloning and expression of human tumor necrosis factor and compariso
A/Reference number: I53311; MUID:86030296; PMID:3932069
A/Accession: I53311
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-233 <MAR>

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A:Cross-references: GB:M26331; NID:G339763; PIDN:AAA36758.1; PID:G339764
A:Experimental source: U-937 cells
R:Takekura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A:Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A:Reference number: S62610; MUID:96202967; PMID:8631363
A:Accession: S62610
A:Molecule type: protein
A:Residues: 77-99 <TAK>
R:D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter region
A:Reference number: I54522; MUID:94102809; PMID:7903959
A:Accession: I54522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <DAL>
A:Cross-references: GB:S68530; NID:G544751
R:Stevenson, F.T.; Bureten, S.L.; Lockley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysine
A:Reference number: A59165; MUID:93018820; PMID:1402651
A:Contents: annotation; identification of myristylated lysines
R:Aggarwal, B.B.; Kohr, W.J.; Haas, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Brink
J. Biol. Chem. 260, 2345-2354, 1985
A:Title: Human tumor necrosis factor. Production, purification, and characterization.
A:Reference number: A92511; MUID:8510974; PMID:3871770
A:Contents: annotation; disulfide bond
C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction
out detriment to normal cells. It can also act synergistically with interferon gamma to
C:Comment: TNF-alpha and -beta (lymphocokine) are the products of different genes closely
related and are produced by different cell types and have different induction kinetics.
C:Genetics:
A:Gene: GDB:TNF, TNFA
A:Cross-references: GDB:120441; OMIM:191160
A:Map position: 6p21.3-6p21.3
A:Introns: 62/3; 78/1; 94/1
C:Complex: homotrimer
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxic; glycoprotein; homotrimer; lipoprotein; lymphokine; macrophage
F:1-76/Domain: propeptide #status predicted <PRO>
F:77-233/Product: tumor necrosis factor #status experimental <MAT>
F:19,20/Binding site: myristate (Lys) (covalent) #status experimental
F:81/Binding site: carbohydrate (Ser) (partial) #status experimental
F:145-177/Disulfide bonds: #status experimental

Query Match 8.5%; Score 125.5; DB 1; Length 233;
Best Local Similarity 17.8%; Pred. No. 0.0036;
Matches 51; Conservative 52; Mismatches 99; Indels 85; Gaps 9;

QY 2 AMMEVGGPSLGGTCVLYIVFTVLIQSLCAVAVTYVFTNELKQMODKSKSGIACFLKED 61
DB 16 ALPKTTGGGQSRRCFLFSFLVAGATTLFCULHFGVIGPQREFFPR----- 65
QY 62 DSYMPNDESNPCWQVQKQWLRQVRCMLRTSEETISTVQEKQKQNTSPLVREKQPR 121
DB 66 -----DLSLISPLAQ-----VRSSSRTPS-----DK 87
QY 122 VAAHITGRGRNLTSSPNSKNEKALGRKINSMESSRSGHSLSLHLNGLVYIHEKGF 181
DB 88 PVAHVVA-----NPAEGQL--QWLNRNAVALLANGVELADNQLVPSSEGL 131
QY 182 YTIYQTVFRFOEIKENTKNDKQNVQYIKYT-----SYDPILIMKSARNSCSK-- 233
DB 132 YLIYQVLFKQ-----GCPSTHVLLTHTISRIAVSYQTKVNLISAIKSPCORETP 182
QY 234 ---DAEYGLYSIYGGIFELKENDRIFFVSTNEHLIDMDHSA--FRG 276
DB 183 EGAERAKPWTEPIYLGQVFLQEKDRLSAETINRPDIYIDPRAESGVYFG 229

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